

SEQUENCE LISTING

<110> Institut Pasteur

<110> Bayer CropScience SA

<120> Mutagenesis of *Aspergillus* fungi and genes essential for growth

<130> D20128

<150> US 60/363 543

<151> 2002-03-13

<150> US 60/434 407

<151> 2002-12-19

<160> 199

<170> PatentIn Ver. 3.2

<210> 1

<211> 2802

<212> DNA

<213> *Aspergillus fumigatus*

<400> 1

```

atgcctcacc ggcgcggcatc cccagcgggtg tcggaaaatg agttcgacat cacaggcgct 60
ctcttccaga acgacagcga ctccgacaac gaacagccct cggccaagtc caaacgacaa 120
cctccgaaga aggttccctc gcaggcgctc gacttcctcg gcgatgtgaa tgaagacgac 180
aatgacgacg aggtctttat tgccgagcag caaacttctg ccaaccgcaa ggctcgaat 240
ctcaaagggt gcaactgtta gaaagggtgg ggtttccaag ccatgggctt gagtgccaat 300
ctgttaaagg caatcgctcg gaaaggcttc tcggatccga ctccattca gcgcaagacc 360
attcccgcta ttatggacga ccaggatgta gttggtatgg cacggactgg ttcaggaaaag 420
acggccgctt tcgttatccc aatgatcgag aaattgaaga gccatagcac caagggtgga 480
gcccgcggtc tggctctgtc cccatcgaga gagctggcac tgcagacatt gaaagtcgtc 540
aaggaaactg gtagaggcac tgacctgaag tcggttcttc ttggtgggtg agacagcctg 600
gaggagcaat tcgcgatgat cgccggcaat ccagatatta ttattgcaac acctggctga 660
ttcctgcatt tgaagggtgga aatgaacctg gacttgctca gtatccgcta tgcgttttc 720
gacgaggctg atcgactggt tgagatgggt ttgcgcgcgc aactaacaga gattttgcac 780
ggctctctcg cgaatcgga gactctctcg ttctctgcca ctcttccgaa gtccctgtc 840
gagtcttccc gcgcggctt gcaggaacct acactagtc gtctggatac cgagagcaag 900
atctcgccc atcttcagaa tgctttcttc tctgtgaaat cctcagagaa ggaaggggcc 960
ttgctctaca tcttcatga ggtcatcaag atgccgactg ggccaaccga ggtttcgcaa 1020
caaaggaaa aagaagatgc aagcgccaag aacttgaaga acaagaagag gaagagagcg 1080
gaaatggaga aggtgtgcaa tacgagagag tctccaacca agcattcgac aatcgttttt 1140
gccgcgacga agcaccatgt cgattatctt tactcactac tctgcgaggc gggattcgcc 1200
gtctcctacg tttacggctc tttagatcaa accgcccga agatccaggt tcaaaacttt 1260
agaacgggca tgaccaatat cctcgttgtc accgacgttg cggctagagg tattgatatt 1320
cctatcctgg caaatgtcat taattacgat tccccctccc agccaaagat ttttgttcac 1380
cggtctcgcc gaactgctcg tgccggggcg aagggtgga gttacagtct ggtccgcgat 1440
gcagacgctc cttatttact tgatttgcaa ctattcctag gaagaaggct ggttggtggc 1500
cgcaattcgg gggatcaagt gaacttcgcc gaagacgttg taacgggcag tctacctagg 1560
gatgggctct ctcaaagctg tgagtgggta accaaggctc tggacgataa tgcagacctt 1620
gcagcccaac gcacggctcg tgctaagggt gagaagctct atatgcgaac ccggaacgcg 1680
gcatctcttg agagtgcgaa gcgatcgaaa cagggtggtt ctccgacaa ttggacaagc 1740
gtacaccgcg tcttccaaga tgaaactagt aatctggagg cggagcggga gaagatgctc 1800
gcccgtattg gtggttaccg gccgccagag acaatctttg aggtcaacaa ccggcggatg 1860
ggcaaacatg agaactgcga cgctctcgat acgattaaga gatttcgtag cactctagag 1920
tccaagaaga agcgtgcaca agcgaatgaa aagtccgagt tctcgaaga cgggtcccgac 1980
gacggaaagg cagtcaacga agccaaagaa accgagagcg agggagcatt ttctgatgag 2040
gacgacgacg ttcccaccgg cgtggcagat aacatgtcga tggcatccga ttcagagctg 2100

```

gaagtcacct	tctcgtcata	ttcaaaatca	aaggacaaca	aggcgaagaa	agcgagcgcg	2160
gcattctttcc	agaaccctga	atacttcatg	tcctataccc	cgaataaacac	ctccctggcg	2220
gaggaccgag	cttatgggtg	gcattccggg	accaactcca	acttcgcccc	ggcctcacgc	2280
agcgcgacca	tggatctggc	aggcgacgat	ggaggcccg	ggttcggcga	ggctcgtacg	2340
ctgatgcgct	gggacaagcg	acacaagaag	tacgtggctc	gacagaatga	cgaggacggc	2400
tccaagggca	cacgcctcgt	ccgcggtgag	agcggggcga	agatcgcagc	cagcttcccg	2460
agcggacggg	tcgacgcttg	gaagagagaa	aatcgtctcg	gccgcttgcc	tcgggtgggt	2520
gaggccgaag	ctgctaattct	cgctgctggt	ctcaacgcag	ccatctcagg	caagcgggtc	2580
aggcatcgca	aggagcaggc	gccccagaag	gctgatcctc	tccgtggtga	ttacgagaag	2640
atgaagaaga	aggctgaact	cgccaaggag	cgagcaatgt	ctaaggctgg	cggcgctgca	2700
ccacgtggca	agagcgagct	gaagagtacg	gacgatatcc	ggattgcgcg	caaattgaag	2760
cagaagagac	gagagaagaa	tgctcgtccc	tcgaggaaga	ag		2802

<210> 2

<211> 2802

<212> DNA

<213> *Aspergillus fumigatus*

<400> 2

atgcctcacc	gcgcggcatc	cccagcgggtg	tcggaaaatg	agttcgacat	cacaggcgct	60
ctcttccaga	acgacagcga	ctccgacaac	gaacagccct	cggccaagtc	caaacgacaa	120
cctccgaaga	aggttccctc	gcaggcgctc	gacttccctc	gcgatgtgaa	tgaagacgac	180
aatgacgacg	aggcttttat	tgccgagcag	caaacttctg	ccaaccgcaa	ggcctcgaat	240
ctcaaagggtc	gcactgttaa	gaaggggtggt	ggtttccaag	ccatgggctt	gagtgccaat	300
ctgttaaagg	caatcgctcg	gaaaggcttc	tcggtaccga	ctcccattca	gcgcaagacc	360
attcccgtta	ttatggacga	ccaggatgta	gttgggtatgg	cacggactgg	ttcaggaaag	420
acggccgctt	tcgttatccc	aatgatcgag	aaattgaaga	gccatagcac	caaggttggg	480
gcccgcgggtc	tggtcttgct	cccacgaga	gagctggcac	tgacagacatt	gaaagtcgtc	540
aaggaactgg	gtagaggcac	tgacctgaag	tcggttcttc	ttgttggtgg	agacagcctg	600
gaggagcaat	tcgcgatgat	cgccggcaat	ccagatatta	ttattgcaac	acctggtcga	660
ttcctgcatt	tgaagggtgga	aatgaacctg	gacttgtcca	gtatccgcta	tgctgttttc	720
gacgaggctg	atcgactggt	tgagatgggt	ttcgccgcgc	aactaacaga	gattttgcac	780
ggtcttccctg	cgaatcggca	gactctcctg	ttctctgcca	ctcttccgaa	gtcccttgct	840
gagtttgccc	gcgcccggctt	gcaggaacct	acactagtcc	gtctggatac	cgagagcaag	900
atctcgcccc	atcttcagaa	tgctttcttc	tctgtgaaat	cctcagagaa	ggaaggggcc	960
ttgctctaca	tccttcatga	ggtcatcaag	atgccgactg	ggccaaccga	ggtttcgcaa	1020
caaaggaag	aagaagatgc	aagcgccaag	aacttgaaga	acaagaagag	gaagagagcg	1080
gaaatggaga	aggctgtcaa	tacgagagag	tctccaacca	agcattcgac	aatcgttttt	1140
gccgcgacga	agcaccatgt	cgattatctt	tactcactac	tctgcgaggc	gggattcgcc	1200
gtctcctacg	tttacggctc	tttagatcaa	accgcccga	agatccaggt	tcaaaacttt	1260
agaacgggca	tgaccaatat	cctcgttgtc	accgacgttg	cggctagagg	tattgatatt	1320
cctatcctgg	caaattgtcat	taattacgat	ttccctccc	agccaaagat	ttttgttcac	1380
cgtgtcggcc	gaactgctcg	tgccggggcg	aagggtcgga	gttacagtct	ggtccgcat	1440
gcagacgctc	cttatttact	tgatttgcaa	ctattcctag	gaagaaggct	ggttggtggc	1500
cgcgaaattcg	gggatcaagt	gaacttcgcc	gaagacgttg	taacgggcag	tctacctagg	1560
gatgggctct	ctcaaagctg	tgagtgggta	accaagggtcc	tggaacgataa	tgacagacct	1620
gcagcccaac	gcacggtcgc	tgctaagggt	gagaagctct	atatgcgaac	ccggaacgcg	1680
gcattctcttg	agagtgcgaa	gcgatcgaaa	cagggtggtt	cttccgacaa	ttggacaagc	1740
gtacacccgc	tcttccaaga	tgaaactagt	aatctggagg	ccgagcggga	gaagatgctc	1800
gcccgtattg	gtgggttaccg	gccgccagag	acaatctttg	aggtaacaa	ccggcggatg	1860
ggcaaacatg	agaacgtcga	cgctctcgat	acgattaaga	gagttcgtag	cactctagag	1920
tccaagaaga	agcgtgcaca	agcgaatgaa	aagtccgagt	tcctcgaaga	cggtcccgcg	1980
gacggaaagg	cagtcacga	agccaaagaa	accgagagcg	aggagcatt	ttctgatgag	2040
gacgacgacg	ttcccaccgg	cgtggcagat	aactgtcgga	tgccatccga	ttcagagctg	2100
gaagtcaacct	tctcgtcata	ttcaaaatca	aaggacaaca	aggcgaagaa	agcgagcgcg	2160
gcattctttcc	agaaccctga	atacttcatg	tcctataccc	cgaataaacac	ctccctggcg	2220
gaggaccgag	cttatgggtg	gcattccggg	accaactcca	acttcgcccc	ggcctcacgc	2280
agcgcgacca	tggatctggc	aggcgacgat	ggaggcccg	ggttcggcga	ggctcgtacg	2340
ctgatgcgct	gggacaagcg	acacaagaag	tacgtggctc	gacagaatga	cgaggacggc	2400
tccaagggca	cacgcctcgt	ccgcggtgag	agcggggcga	agatcgcagc	cagcttcccg	2460

```

agcggacggt tcgacgcttg gaagagagaa aatcgtctcg gccgcttgcc tcgggtgggt 2520
gaggccgaag ctgctaactt cgctgctggg ctcaacgcag ccatctcagg caagcggttc 2580
aggcatcgca aggagcaggc gcccaagaag gctgatactc tccgtgggtga ttacgagaag 2640
atgaagaaga aggctgaact cgccaaggag cgagcaatgt ctaaggctgg cggcgctgca 2700
ccacgtggca agagcgagct gaagagtacg gacgatatcc ggattgcgcg caaattgaag 2760
cagaagagac gagagaagaa tgctcgtccc tcgaggaaga ag 2802

```

<210> 3

<211> 934

<212> PRT

<213> *Aspergillus fumigatus*

<400> 3

```

Met Pro His Arg Ala Ala Ser Pro Ala Val Ser Glu Asn Glu Phe Asp
  1              5              10              15

Ile Thr Gly Ala Leu Phe Gln Asn Asp Ser Asp Ser Asp Asn Glu Gln
          20              25              30

Pro Ser Ala Lys Ser Lys Arg Gln Pro Pro Lys Lys Val Pro Ser Gln
          35              40              45

Ala Leu Asp Phe Leu Gly Asp Val Asn Glu Asp Asp Asn Asp Asp Glu
  50              55              60

Ala Phe Ile Ala Glu Gln Gln Thr Ser Ala Asn Arg Lys Ala Ser Asn
  65              70              75              80

Leu Lys Gly Arg Thr Val Lys Lys Gly Gly Gly Phe Gln Ala Met Gly
          85              90              95

Leu Ser Ala Asn Leu Leu Lys Ala Ile Ala Arg Lys Gly Phe Ser Val
          100             105             110

Pro Thr Pro Ile Gln Arg Lys Thr Ile Pro Val Ile Met Asp Asp Gln
          115             120             125

Asp Val Val Gly Met Ala Arg Thr Gly Ser Gly Lys Thr Ala Ala Phe
          130             135             140

Val Ile Pro Met Ile Glu Lys Leu Lys Ser His Ser Thr Lys Val Gly
          145             150             155             160

Ala Arg Gly Leu Val Leu Ser Pro Ser Arg Glu Leu Ala Leu Gln Thr
          165             170             175

Leu Lys Val Val Lys Glu Leu Gly Arg Gly Thr Asp Leu Lys Ser Val
          180             185             190

Leu Leu Val Gly Gly Asp Ser Leu Glu Glu Gln Phe Ala Met Ile Ala
          195             200             205

Gly Asn Pro Asp Ile Ile Ile Ala Thr Pro Gly Arg Phe Leu His Leu
          210             215             220

Lys Val Glu Met Asn Leu Asp Leu Ser Ser Ile Arg Tyr Val Val Phe
          225             230             235             240

Asp Glu Ala Asp Arg Leu Phe Glu Met Gly Phe Ala Ala Gln Leu Thr
          245             250             255

```

Glu Ile Leu His Gly Leu Pro Ala Asn Arg Gln Thr Leu Leu Phe Ser
 260 265 270
 Ala Thr Leu Pro Lys Ser Leu Val Glu Phe Ala Arg Ala Gly Leu Gln
 275 280 285
 Glu Pro Thr Leu Val Arg Leu Asp Thr Glu Ser Lys Ile Ser Pro Asp
 290 295 300
 Leu Gln Asn Ala Phe Phe Ser Val Lys Ser Ser Glu Lys Glu Gly Ala
 305 310 315 320
 Leu Leu Tyr Ile Leu His Glu Val Ile Lys Met Pro Thr Gly Pro Thr
 325 330 335
 Glu Val Ser Gln Gln Arg Lys Glu Glu Asp Ala Ser Ala Lys Asn Leu
 340 345 350
 Lys Asn Lys Lys Arg Lys Arg Ala Glu Met Glu Lys Ala Val Asn Thr
 355 360 365
 Arg Glu Ser Pro Thr Lys His Ser Thr Ile Val Phe Ala Ala Thr Lys
 370 375 380
 His His Val Asp Tyr Leu Tyr Ser Leu Leu Cys Glu Ala Gly Phe Ala
 385 390 395 400
 Val Ser Tyr Val Tyr Gly Ser Leu Asp Gln Thr Ala Arg Lys Ile Gln
 405 410 415
 Val Gln Asn Phe Arg Thr Gly Met Thr Asn Ile Leu Val Val Thr Asp
 420 425 430
 Val Ala Ala Arg Gly Ile Asp Ile Pro Ile Leu Ala Asn Val Ile Asn
 435 440 445
 Tyr Asp Phe Pro Ser Gln Pro Lys Ile Phe Val His Arg Val Gly Arg
 450 455 460
 Thr Ala Arg Ala Gly Arg Lys Gly Trp Ser Tyr Ser Leu Val Arg Asp
 465 470 475 480
 Ala Asp Ala Pro Tyr Leu Leu Asp Leu Gln Leu Phe Leu Gly Arg Arg
 485 490 495
 Leu Val Val Gly Arg Glu Phe Gly Asp Gln Val Asn Phe Ala Glu Asp
 500 505 510
 Val Val Thr Gly Ser Leu Pro Arg Asp Gly Leu Ser Gln Ser Cys Glu
 515 520 525
 Trp Val Thr Lys Val Leu Asp Asp Asn Ala Asp Leu Ala Ala Gln Arg
 530 535 540
 Thr Val Ala Ala Lys Gly Glu Lys Leu Tyr Met Arg Thr Arg Asn Ala
 545 550 555 560
 Ala Ser Leu Glu Ser Ala Lys Arg Ser Lys Gln Val Val Ser Ser Asp
 565 570 575

Asn Trp Thr Ser Val His Pro Leu Phe Gln Asp Glu Thr Ser Asn Leu
 580 585 590
 Glu Ala Glu Arg Glu Lys Met Leu Ala Arg Ile Gly Gly Tyr Arg Pro
 595 600 605
 Pro Glu Thr Ile Phe Glu Val Asn Asn Arg Arg Met Gly Lys His Glu
 610 615 620
 Asn Val Asp Ala Leu Asp Thr Ile Lys Arg Val Arg Ser Thr Leu Glu
 625 630 635 640
 Ser Lys Lys Lys Arg Ala Gln Ala Asn Glu Lys Ser Glu Phe Leu Glu
 645 650 655
 Asp Gly Pro Asp Asp Gly Lys Ala Val Asn Glu Ala Lys Glu Thr Glu
 660 665 670
 Ser Glu Gly Ala Phe Ser Asp Glu Asp Asp Asp Val Pro Thr Gly Val
 675 680 685
 Ala Asp Asn Met Ser Met Ala Ser Asp Ser Glu Leu Glu Val Thr Phe
 690 695 700
 Ser Ser Tyr Ser Lys Ser Lys Asp Asn Lys Ala Lys Lys Ala Ser Ala
 705 710 715 720
 Ala Ser Phe Gln Asn Pro Glu Tyr Phe Met Ser Tyr Thr Pro Asn Asn
 725 730 735
 Thr Ser Leu Ala Glu Asp Arg Ala Tyr Gly Val His Ser Gly Thr Asn
 740 745 750
 Ser Asn Phe Ala Gln Ala Ser Arg Ser Ala Thr Met Asp Leu Ala Gly
 755 760 765
 Asp Asp Gly Gly Arg Gly Phe Gly Glu Ala Arg Thr Leu Met Arg Trp
 770 775 780
 Asp Lys Arg His Lys Lys Tyr Val Ala Arg Gln Asn Asp Glu Asp Gly
 785 790 795 800
 Ser Lys Gly Thr Arg Leu Val Arg Gly Glu Ser Gly Ala Lys Ile Ala
 805 810 815
 Ala Ser Phe Arg Ser Gly Arg Phe Asp Ala Trp Lys Arg Glu Asn Arg
 820 825 830
 Leu Gly Arg Leu Pro Arg Val Gly Glu Ala Glu Ala Ala Asn Leu Ala
 835 840 845
 Ala Gly Leu Asn Ala Ala Ile Ser Gly Lys Arg Phe Arg His Arg Lys
 850 855 860
 Glu Gln Ala Pro Lys Lys Ala Asp Pro Leu Arg Gly Asp Tyr Glu Lys
 865 870 875 880
 Met Lys Lys Lys Ala Glu Leu Ala Lys Glu Arg Ala Met Ser Lys Ala
 885 890 895

Gly Gly Ala Ala Pro Arg Gly Lys Ser Glu Leu Lys Ser Thr Asp Asp
 900 905 910

Ile Arg Ile Ala Arg Lys Leu Lys Gln Lys Arg Arg Glu Lys Asn Ala
 915 920 925

Arg Pro Ser Arg Lys Lys
 930

<210> 4

<211> 1735

<212> DNA

<213> *Aspergillus fumigatus*

<400> 4

atgagtgc	aa	tcctttctgc	agacgatttg	aacgattttca	tttctcccgg	ggttgcttgc	60
atcaagccc	g	ttgagagtct	accacaaaaa	gaatcccagt	cggaggtatc	tttcctgtct	120
taccagtcat	t	ctgttgatat	cagccaatag	gctaacgctc	atttccaatt	caatagaatc	180
cctatgaggt	g	gacaaaaggaa	gacaaaagttc	aaccggaaaa	ccttcccccg	gctcagattt	240
cattgactga	t	ttgccttgca	tgctccggat	gtgtcacgtc	tgcggaagca	gtgttgatat	300
ccttgcaatc	a	acatacggag	gttctcaata	ctcttgattc	gtacccccga	ttgccgcttg	360
gttctacaag	a	ctaccaaaga	ggcacacaaa	aagttggatc	agcagacagc	gatggtcgca	420
tctttgttgc	t	tagcgtcagc	cctcaagtca	gggcgagctt	ggcagccaca	tacggaatca	480
ccgagcggga	g	ggcgaaatat	atgattgacc	aatttcttat	gggccctcac	ggtctcagag	540
ctggtggaaa	a	acatggcaat	gggtttacat	gggttggtga	cacgaacgtt	atgcgtgaag	600
cagtgttggc	t	tctgacagcg	gacgaggtca	cgagctcttt	attatcaact	ggatcgggca	660
gccttcccaa	a	gagtccaatt	ctttcgctcg	cttgccccgg	ctggatatgt	tatgctgaaa	720
aaacacaccc	t	ttttatcctt	ccgcatttat	ctcgccctcaa	gtctcctcag	gcgttgagcg	780
gcacatttct	t	gaagtccagt	ctaagcaagg	cacttggggt	cccgccttct	cagatatggc	840
atttagctat	t	catgccatgc	ttcgacaaga	agctggaagc	tagccgggaa	gagctgacag	900
acattgcatg	g	ggcttcaacc	ttcaccacag	cacagacaac	acccgtccgc	gacgttgact	960
gtgtcataac	a	caccctgtag	ctactaactt	tagccactgc	taggggggct	tctctaccca	1020
atttgccgct	t	caaaccattg	cccgcgctcat	gttttaactcc	atttccagat	caagccctag	1080
aatcattttt	t	gttctctaag	agctcgctcg	gccaaacagt	cgaatcaggg	acatctggag	1140
gctatcttca	t	tcacgtcctc	caaactcttc	aagccagaaa	ccccggcagc	aagattgtca	1200
cccagcgttg	g	gcgcaacgcc	gatgttggtg	aatatgtgct	catgtcgtct	ggggatgagc	1260
ctctttttag	t	ggcggctcgg	tattatggct	tcaggaatat	acaaaatctc	gtcagaaaac	1320
ttaaaccgcg	c	acgcgtgtca	agactgccag	gcgccaagcc	gcaagcggtc	tcttcaagtg	1380
caaatcgacg	a	acagcccatg	tcaaggaacg	cagctccggc	tggaacaggc	gctgattatg	1440
catatgttga	t	agtcatggct	tgtcctggcg	gctgtaccaa	tggtggtggg	caaataagga	1500
ttgaagatgc	c	ccgggaggct	gttccgaacg	cactaaaaga	gacatcgact	gaaactcctg	1560
tggtgcacc	a	gaaacccacg	ccgcatgagc	agcgtgctg	gctagcccgg	gtagatgaag	1620
cgtactactc	t	tgccgactcg	gatagcgagg	gatctgtcac	gacggagccg	gtttctgtcc	1680
tgtcaaggga	a	taaccagatt	catgagtttt	tgaactattg	gtcagagaag	gttga	1735

<210> 5

<211> 1592

<212> DNA

<213> *Aspergillus fumigatus*

<400> 5

atgagtgc	aa	tcctttctgc	agacgatttg	aacgattttca	tttctcccgg	ggttgcttgc	60
atcaagccc	g	ttgagagtct	accacaaaaa	gaatcccagt	cggagaaatc	ctatgaggtg	120
acaaaggaag	a	acaaagttca	accggaaaac	cttcccccg	ctcagatttc	attgactgat	180
tgcttgc	a	gctccggatg	tgctcacgtc	gcggaagcag	tggtgatata	cttgcaatca	240
catacggagg	g	ttctcaatac	tcttgattcc	gatggtcgca	tctttgttgc	tagcgtcagc	300
cctcaagtca	a	gggcgagctt	ggcagccaca	tacggaatca	ccgagcggga	ggcgaaatat	360
atgattgacc	a	aatttcttat	gggccctcac	ggtctcagag	ctggtggaaa	acatggcaat	420

```

gggtttacat gggttgtgga cacgaacggt atgcgtgaag cagtgttggc tctgacagcg 480
gacgaggtca cgagctcttt attatcaact ggatcgggca gccttcccaa gagtccaatt 540
ctttcgtccg cttgccccgg ctggatatgt tatgctgaaa aaacacacccc ttttatcctt 600
ccgcatttat ctgcctcaa gtctcctcag gcgttgagcg gcacatttct gaagtcagtg 660
ctaagcaagg cacttggggt cccgccttct cagatatggc atttagctat catgccatgc 720
ttcgacaaga agctggaagc tagccgggaa gagctgacag acattgcatg ggcttcaacc 780
ttcaccaggt cacagacaac acccgtccgc gacgttgact gtgtcataac caccctgag 840
ctactaactt tagccactgc tagggggcct tctctaccca atttgccgct caaaccattg 900
cccgcgtcat gtttaactcc atttccagat caagccctag aatcattttt gttctctaag 960
agctcgtcgg gccaaacagt cgaatcaggg acatctggag gctatcttca tcacgtcctc 1020
caaattcttc aagccagaaa ccccggcagc aagattgtca ccagcgtgg gcgcaacgcc 1080
gatgttgttg aatatgtgct catgtcgtct ggggatgagc ctcttttttag ggcggtcgg 1140
tattatggct tcaggaatat acaaaatctc gtcagaaaac ttaaaccgc acgcgtgtca 1200
agactgccag gcgccaagcc gcaagcggtc tcttcaagt caaatcgac acagcccatg 1260
tcaaggaacg cagctccggc tggaacaggc gctgattat catatgttga agtcatggct 1320
tgtcctggcg gctgtaccaa tgggtggggg caaataagga ttgaagatgc ccgggaggct 1380
gttccgaacg cactaaaaga gacatcgact gaaactcctg tggctgcacc gaaaccacg 1440
ccgcatgagc agcgtgcctg gctagcccgg gtagatgaag cgtactactc tgcggactcg 1500
gatagcgagg gatctgtcac gacggagccg gtttctgtcc tgtcaaggga taaccagatt 1560
catgagtttt tgaactattg gtcagagaag gt 1592

```

<210> 6

<211> 530

<212> PRT

<213> *Aspergillus fumigatus*

<400> 6

```

Met Ser Ala Ile Leu Ser Ala Asp Asp Leu Asn Asp Phe Ile Ser Pro
  1             5             10             15

```

```

Gly Val Ala Cys Ile Lys Pro Val Glu Ser Leu Pro Gln Lys Glu Ser
          20             25             30

```

```

Gln Ser Glu Asn Pro Tyr Glu Val Thr Lys Glu Asp Lys Val Gln Pro
      35             40             45

```

```

Glu Asn Leu Pro Pro Ala Gln Ile Ser Leu Thr Asp Cys Leu Ala Cys
      50             55             60

```

```

Ser Gly Cys Val Thr Ser Ala Glu Ala Val Leu Ile Ser Leu Gln Ser
      65             70             75             80

```

```

His Thr Glu Val Leu Asn Thr Leu Asp Ser Asp Gly Arg Ile Phe Val
          85             90             95

```

```

Ala Ser Val Ser Pro Gln Val Arg Ala Ser Leu Ala Ala Thr Tyr Gly
      100             105             110

```

```

Ile Thr Glu Arg Glu Ala Lys Tyr Met Ile Asp Gln Phe Leu Met Gly
      115             120             125

```

```

Pro His Gly Leu Arg Ala Gly Gly Lys His Gly Asn Gly Phe Thr Trp
      130             135             140

```

```

Val Val Asp Thr Asn Val Met Arg Glu Ala Val Leu Ala Leu Thr Ala
      145             150             155             160

```

```

Asp Glu Val Thr Ser Ser Leu Leu Ser Thr Gly Ser Gly Ser Leu Pro
          165             170             175

```

Lys Ser Pro Ile Leu Ser Ser Ala Cys Pro Gly Trp Ile Cys Tyr Ala
 180 185 190
 Glu Lys Thr His Pro Phe Ile Leu Pro His Leu Ser Arg Leu Lys Ser
 195 200 205
 Pro Gln Ala Leu Ser Gly Thr Phe Leu Lys Ser Val Leu Ser Lys Ala
 210 215 220
 Leu Gly Val Pro Pro Ser Gln Ile Trp His Leu Ala Ile Met Pro Cys
 225 230 235 240
 Phe Asp Lys Lys Leu Glu Ala Ser Arg Glu Glu Leu Thr Asp Ile Ala
 245 250 255
 Trp Ala Ser Thr Phe Thr Gln Ser Gln Thr Thr Pro Val Arg Asp Val
 260 265 270
 Asp Cys Val Ile Thr Thr Arg Glu Leu Leu Thr Leu Ala Thr Ala Arg
 275 280 285
 Gly Leu Ser Leu Pro Asn Leu Pro Leu Lys Pro Leu Pro Ala Ser Cys
 290 295 300
 Leu Thr Pro Phe Pro Asp Gln Ala Leu Glu Ser Phe Leu Phe Ser Lys
 305 310 315 320
 Ser Ser Ser Gly Gln Thr Val Glu Ser Gly Thr Ser Gly Gly Tyr Leu
 325 330 335
 His His Val Leu Gln Ile Phe Gln Ala Arg Asn Pro Gly Ser Lys Ile
 340 345 350
 Val Thr Gln Arg Gly Arg Asn Ala Asp Val Val Glu Tyr Val Leu Met
 355 360 365
 Ser Ser Gly Asp Glu Pro Leu Phe Arg Ala Ala Arg Tyr Tyr Gly Phe
 370 375 380
 Arg Asn Ile Gln Asn Leu Val Arg Lys Leu Lys Pro Ala Arg Val Ser
 385 390 395 400
 Arg Leu Pro Gly Ala Lys Pro Gln Ala Val Ser Ser Ser Ala Asn Arg
 405 410 415
 Arg Gln Pro Met Ser Arg Asn Ala Ala Pro Ala Gly Thr Gly Ala Asp
 420 425 430
 Tyr Ala Tyr Val Glu Val Met Ala Cys Pro Gly Gly Cys Thr Asn Gly
 435 440 445
 Gly Gly Gln Ile Arg Ile Glu Asp Ala Arg Glu Ala Val Pro Asn Ala
 450 455 460
 Leu Lys Glu Thr Ser Thr Glu Thr Pro Val Ala Ala Pro Lys Pro Thr
 465 470 475 480
 Pro His Glu Gln Arg Ala Trp Leu Ala Arg Val Asp Glu Ala Tyr Tyr
 485 490 495
 Ser Ala Asp Ser Asp Ser Glu Gly Ser Val Thr Thr Glu Pro Val Ser

500

505

510

Val Leu Ser Arg Asp Asn Gln Ile His Glu Phe Leu Asn Tyr Trp Ser
 515 520 525

Glu Lys
 530

<210> 7

<211> 942

<212> DNA

<213> *Aspergillus fumigatus*

<400> 7

```

atgactaccg gggctggtac gatctctcat tccaacacct atcatcgtat tcctcgccgt 60
taactgacca atccaccagt gcaaagggtc cgtccagtgg tggatcggg tccctctggg 120
actgggaagt cgaccttgct caagagactc ttcgctgaat accccgatac ttctgattta 180
tccgtgtctc gtacgtctaa ccccttgcca accctcattg actatgcctg cgaattgttt 240
cttttggtgg aattgcgctg aacgggtgtt gttatattta gataccactc gagctccccg 300
tccccgggaa gaaaatggac gtgagtatta cttcacaact aaagaagatt tcctggatct 360
tgtgagcaag aatgccttta tcgagcatgc gcagtttggt ggcaattact acggtactac 420
tgtgcaggca gtgaaggatg ttgcgcagaa gggcaagatc tgcgttctcg acattgagat 480
gaggtaataa tagtcctgca acgtgaactg atatgaccgg agaagcagag gaaatccatc 540
atcaaattgga ttgtagttca acccaaacaa cagctgacga ctgaattgca atagggcgtg 600
aaacaagtca agcgcaccga tcttgatgct cgattcttat ttttagcacc cccgtccctt 660
gaagaactag agaaaagact gcgtgggaga gcaaccgaga ctgaggagag cttgacggta 720
tggctgtcct ccacattcct tcacttcccc aactcgccag actgtcccgc tgggaattcta 780
actttgcgtc agaaacgcct tgcccaagct aaaaatgaat tgggaatatgc ggcgcagcct 840
ggctctcatg ataagattgt cgtgaacgat gacctggaga aggcttataa ggaactgcgg 900
gattggattg tcgacggtgg taactttgga gcgcgtcaat ga 942

```

<210> 8

<211> 600

<212> DNA

<213> *Aspergillus fumigatus*

<400> 8

```

atgactaccg gggctgtgca aaggttccgt ccagtgggtg tatcgggtcc ctctgggact 60
gggaagtcga ccttgctcaa gagactcttc gctgaatacc ccgatacttt cgatttatcc 120
gtgtctcata ccaactcgagc tccccgtccc ggggaagaaa atggacgtga gtattacttc 180
acaactaaag aagatttcct ggatcttggt agcaagaatg cctttatcga gcatgcgcag 240
tttggtggca attactacgg tactactgtg caggcagtga aggatgttgc gcagaagggc 300
aagatctgcy ttctcgacat tgagatgagg ggcgtgaaac aagtcaagcg caccgatctt 360
gatgctcgat tcttattttt agcaccctcg tcccttgaaag aactagagaa aagactgcgt 420
gggagagcaa ccgagactga ggagagcttg acgaaacgcc ttgcccagc taaaaatgaa 480
ttggaatatg cggcgcagcc tggctctcat gataagattg tcgtgaacga tgacctggag 540
aaggcttata aggaactgcg ggattggatt gtcgacggtg gtaacttttg agcgcgtcaa 600

```

<210> 9

<211> 200

<212> PRT

<213> *Aspergillus fumigatus*

<400> 9

Met Thr Thr Gly Ala Val Gln Arg Phe Arg Pro Val Val Val Ser Gly
 1 5 10 15

Pro Ser Gly Thr Gly Lys Ser Thr Leu Leu Lys Arg Leu Phe Ala Glu
 20 25 30

Tyr Pro Asp Thr Phe Asp Leu Ser Val Ser His Thr Thr Arg Ala Pro
 35 40 45

Arg Pro Gly Glu Glu Asn Gly Arg Glu Tyr Tyr Phe Thr Thr Lys Glu
 50 55 60

Asp Phe Leu Asp Leu Val Ser Lys Asn Ala Phe Ile Glu His Ala Gln
 65 70 75 80

Phe Gly Gly Asn Tyr Tyr Gly Thr Thr Val Gln Ala Val Lys Asp Val
 85 90 95

Ala Gln Lys Gly Lys Ile Cys Val Leu Asp Ile Glu Met Arg Gly Val
 100 105 110

Lys Gln Val Lys Arg Thr Asp Leu Asp Ala Arg Phe Leu Phe Leu Ala
 115 120 125

Pro Pro Ser Leu Glu Glu Leu Glu Lys Arg Leu Arg Gly Arg Ala Thr
 130 135 140

Glu Thr Glu Glu Ser Leu Thr Lys Arg Leu Ala Gln Ala Lys Asn Glu
 145 150 155 160

Leu Glu Tyr Ala Ala Gln Pro Gly Ser His Asp Lys Ile Val Val Asn
 165 170 175

Asp Asp Leu Glu Lys Ala Tyr Lys Glu Leu Arg Asp Trp Ile Val Asp
 180 185 190

Gly Gly Asn Phe Gly Ala Arg Gln
 195 200

<210> 10

<211> 2059

<212> DNA

<213> *Aspergillus fumigatus*

<400> 10

atgttagaag ccttcgaagt cttgacaaca tctgggggtgg tgctgtggtc gaagtcgtat 60
 gcgccggtcg gagcgcatgt tgtcaacagc ctaatcaacg atgtcttcat tgaggagaag 120
 gttcgagcgc agaatcaggc agcgagcagt gcagctccta tctacaagaa ggaaaagtat 180
 actctgaaat ggaagcaagt aaaggatttc aatctgatat ttgtggtatg ttcacgccgc 240
 tcgttgattc aatggcgcca ctgaccgatt ccataggctg tatatcaatc tctgctacat 300
 cttggttgga tcgacaaact cttggataat gtttcgacca tattcatcga cttatataag 360
 gatgagctaa ggagcacacg ggctaggatt attgagtacc cattcgataa gtacttcgac 420
 cagcaggtgc gagagcttga ggacaatgct ggggctccta catcagaatc tctcgtagta 480
 gagatcaacg agagaaagga ccctcttgct tcacagata acggcgggcc acctccgcca 540
 cccgtgcctg gtctgctgaa aggtatctga cgtcgataat ttttctctgc tagtgatcat 600
 attgctaact acctccgaag cgcaacgtcc agttgcgcag ggcgtggcga cctcggacga 660
 gggttcgcca ccccaaacc cagatctttc tcgatcgta acgcccattt caggatcatct 720
 attgaccgcg aaaggagggc ctgctggccg cgcctctcgt cgcgcacgca aagcggccaa 780
 cgcgagcgt accgcttctt ctggagatga aagcattcgg aaggggaaaa cattgaaaag 840
 tggaaaaaag atgcgcaagt gggatgctga tggctttgcg gatgaggacg acggcaaggt 900
 cctcgattac tccgcccccg cagatggtga ggacgcaccg gctcctgtag tcgaggctgt 960
 tgcgcaggaa tcctggggac gccgaacagg caagggccaa tttgtgctga aagatctagg 1020

```

ggatgaagtc cattccattc ttgagaatgc tgatcatgaa aagacaaaagt cttcctcgtc 1080
cacgggcttt gttgggtctg gagtcaacgc acttggtgga ttcttccgta atattgtcgg 1140
cggcaagggtc cttactgagg ctgacttgga gaaacccttg aaagccatgg aagaccattt 1200
gctgaagaag aacggttgcc gcgaagcggc cgtccgtcta tgtcaaggcg tccagcgcga 1260
attagttggc aagaagacag gcaactttca aagtgttgat gcagcactgc gctccgcaat 1320
ggagtccctc ttgcgcaaaa tattgacgcc aacgtcatct ctcgatctac tgcgtgagat 1380
cgatgctgtt agatctccga cgagcaaaag acaggctcct cgcccatatg tcatttccat 1440
cgtgggcgtg aacggtgttg ggaagtcgac aaatctgggc aaaatttgtt acttccttct 1500
ccagaataac tatcgtgttc tgattgcagc ctgtgacacc ttccgctctg gagccgtgga 1560
gcagttacga gtccatgtct gcaatttgaa ggaacttagt acccgggaga atgctggaga 1620
ggttgaactc tacgagaagg gatattgaaa ggaatgcagc aatgtagcga aggatgcagt 1680
ggagtacggt gcggcgaatc atttcgacgt tgtgttgatt gatactgccg gtcgccgtca 1740
taacgaccaa cgccttatgt ctccgctcga gaagtccgcc aagtccgcca aaccagataa 1800
gatcttcatg gtcggtgaag ctctggtcgg tacggacagc gtgatgcagg ctcgcaactt 1860
caaccaagct ttcggcactg ggagaaacct cgatgggttc atcatcagta aatgtgatac 1920
cgttggtgac atggtaggta cgcttgtcag catggtgcat gctacaggca ttcctattgt 1980
ttttctgggt gtaggccagc actatggtga tttgaggggc ctaagtgttc cttgggctgt 2040
caatctgctg atgaagtga 2059

```

<210> 11

<211> 1923

<212> DNA

<213> *Aspergillus fumigatus*

<400> 11

```

atgtagaag ccttcgaagt cttgacaaca tctggggtgg tgctgtggtc gaagtcgtat 60
gcgcgggtcg gagcgcatgt tgtcaacagc ctaatcaacg atgtcttcat tgaggagaag 120
gttcgagcgc agaatacaggc agcgagcagt gcagctccta tctacaagaa ggaaaagtat 180
actctgaaat ggaagcaagt aaaggatttc aatctgatat ttgtggctgt atatcaatct 240
ctgctacatc ttggttggtat cgacaaactc ttggataatg ttccgaccat attcatcgac 300
ttatataagg atgagctaag gagcacacgg gctaggatta ttgagtaccc attcgataag 360
tacttcgacc agcagggtcg agagcttgag gacaatgctg gggctcctac atcagaatct 420
cctccgccac ccgtgcctgt tgcgcagggc gtggcgacct cggacgaggg ttcgccaccc 480
caaacccccg atctttctcg atcgtcaacg cccatttcag gtcacttatt gaccgcgaaa 540
ggagggcctg ctggccgcgc ctctcgctcg gcacgcaaag cggccaacgc gagcgctacc 600
gcttctctcg gagatgaaag cattcggaag gggaaaacat tgaagtggtg aaaaaagatg 660
cgcaagtggg atgctgatgg ctttgcggtat gaggacgacg gcaaggctct cgattactcc 720
gccccgcgag atggtgagga cgcaccggct cctgtagtcg aggctgttgc gcaggaatcc 780
tggggacgcc gaacaggcaa gggccaattt gtgctgaaag atctagggga tgaagtccat 840
tccattcttg agaatgctga tcatgaaaag acaaagtctt cctcgtccac gggctttgtt 900
gggtctggag tcaacgcact tgggtgattc ttccgtaata ttgtcggcgg caaggtcctt 960
actgaggctg acttgagaa acccttgaaa gccatggaag accatttgct gaagaagaac 1020
gttgcgcgcg aagcgccgtt ccgtctatgt caaggcgtcc agcgcgaaat agttggcaag 1080
aagacaggca actttcaaag tgttgatgca gcaactgcgt ccgcaatgga gtctcgttg 1140
cgcaaaatat tgacgccaac gtcactctct gatctactgc gtgagatcga tgctgttaga 1200
tctccgacga gcaaaggaca ggctcctcgc ccatatgtca tttccatcgt gggcgtgaac 1260
ggtgttggga agtcgacaaa tctgggcaaa atttgttact tccttctcca gaataactat 1320
cgtgttctga ttgcagcctg tgacaccttc cgctctggag ccgtggagca gttacgagtc 1380
catgctcgca atttgaagga acttagtacc cgggagaatg ctggagaggt tgaactctac 1440
gagaagggat atggaaagga tgcagcgaat gtagcgaagg atgcagtgga gtacggtcg 1500
gcgaatcatt tcgacgttgt gttgattgat actgcgggtc gccgtcataa cgaccaacgc 1560
cttatgtctt cgctcgagaa ttgcgcaaac ttcgccaac cagataagat cttcatggtc 1620
ggtagaagctc tggtcggtac ggacagcgtg atgcaggctc gcaacttcaa ccaagctttc 1680
ggcactggga gaaacctcga tgggttcatc atcagtaaat gtgataccgt tggtgacatg 1740
gtaggtacgc ttgtcagcat ggtgcatgct acaggcattc ctattgtttt tctgggtgta 1800
ggccagcact atggtgattt gaggggccta agtgctcctt gggctgtcaa tctgctgatg 1860
aag 1923

```

<210> 12

<211> 641

<212> PRT

<213> *Aspergillus fumigatus*

<400> 12

Met Leu Glu Ala Phe Glu Val Leu Thr Thr Ser Gly Val Val Leu Trp
 1 5 10 15

Ser Lys Ser Tyr Ala Pro Val Gly Ala His Val Val Asn Ser Leu Ile
 20 25 30

Asn Asp Val Phe Ile Glu Glu Lys Val Arg Ala Gln Asn Gln Ala Ala
 35 40 45

Ser Ser Ala Ala Pro Ile Tyr Lys Lys Glu Lys Tyr Thr Leu Lys Trp
 50 55 60

Lys Gln Val Lys Asp Phe Asn Leu Ile Phe Val Ala Val Tyr Gln Ser
 65 70 75 80

Leu Leu His Leu Gly Trp Ile Asp Lys Leu Leu Asp Asn Val Ser Thr
 85 90 95

Ile Phe Ile Asp Leu Tyr Lys Asp Glu Leu Arg Ser Thr Arg Ala Arg
 100 105 110

Ile Ile Glu Tyr Pro Phe Asp Lys Tyr Phe Asp Gln Gln Val Arg Glu
 115 120 125

Leu Glu Asp Asn Ala Gly Ala Pro Thr Ser Glu Ser Leu Val Val Glu
 130 135 140

Ile Asn Glu Arg Lys Asp Pro Leu Val Ser Ser Asp Asn Gly Gly Pro
 145 150 155 160

Pro Pro Pro Pro Val Pro Val Ala Gln Gly Val Ala Thr Ser Asp Glu
 165 170 175

Gly Ser Pro Pro Gln Thr Pro Asp Leu Ser Arg Ser Ser Thr Pro Ile
 180 185 190

Ser Gly His Leu Leu Thr Ala Lys Gly Gly Pro Ala Gly Arg Ala Ser
 195 200 205

Arg Arg Ala Arg Lys Ala Ala Asn Ala Ser Ala Thr Ala Ser Ser Gly
 210 215 220

Asp Glu Ser Ile Arg Lys Gly Lys Thr Leu Lys Ser Gly Lys Lys Met
 225 230 235 240

Arg Lys Trp Asp Ala Asp Gly Phe Ala Asp Glu Asp Asp Gly Lys Val
 245 250 255

Leu Asp Tyr Ser Ala Pro Ala Asp Gly Glu Asp Ala Pro Ala Pro Val
 260 265 270

Val Glu Ala Val Ala Gln Glu Ser Trp Gly Arg Arg Thr Gly Lys Gly
 275 280 285

Gln Phe Val Leu Lys Asp Leu Gly Asp Glu Val His Ser Ile Leu Glu

290	295	300
Asn Ala Asp His Glu Lys Thr Lys Ser Ser Ser Ser Thr Gly Phe Val 305 310 315 320		
Gly Ser Gly Val Asn Ala Leu Gly Gly Phe Phe Arg Asn Ile Val Gly 325 330 335		
Gly Lys Val Leu Thr Glu Ala Asp Leu Glu Lys Pro Leu Lys Ala Met 340 345 350		
Glu Asp His Leu Leu Lys Lys Asn Val Ala Arg Glu Ala Ala Val Arg 355 360 365		
Leu Cys Gln Gly Val Gln Arg Glu Leu Val Gly Lys Lys Thr Gly Asn 370 375 380		
Phe Gln Ser Val Asp Ala Ala Leu Arg Ser Ala Met Glu Ser Ser Leu 385 390 395 400		
Arg Lys Ile Leu Thr Pro Thr Ser Ser Leu Asp Leu Leu Arg Glu Ile 405 410 415		
Asp Ala Val Arg Ser Pro Thr Ser Lys Gly Gln Ala Pro Arg Pro Tyr 420 425 430		
Val Ile Ser Ile Val Gly Val Asn Gly Val Gly Lys Ser Thr Asn Leu 435 440 445		
Gly Lys Ile Cys Tyr Phe Leu Leu Gln Asn Asn Tyr Arg Val Leu Ile 450 455 460		
Ala Ala Cys Asp Thr Phe Arg Ser Gly Ala Val Glu Gln Leu Arg Val 465 470 475 480		
His Ala Arg Asn Leu Lys Glu Leu Ser Thr Arg Glu Asn Ala Gly Glu 485 490 495		
Val Glu Leu Tyr Glu Lys Gly Tyr Gly Lys Asp Ala Ala Asn Val Ala 500 505 510		
Lys Asp Ala Val Glu Tyr Gly Ala Ala Asn His Phe Asp Val Val Leu 515 520 525		
Ile Asp Thr Ala Gly Arg Arg His Asn Asp Gln Arg Leu Met Ser Ser 530 535 540		
Leu Glu Lys Phe Ala Lys Phe Ala Lys Pro Asp Lys Ile Phe Met Val 545 550 555 560		
Gly Glu Ala Leu Val Gly Thr Asp Ser Val Met Gln Ala Arg Asn Phe 565 570 575		
Asn Gln Ala Phe Gly Thr Gly Arg Asn Leu Asp Gly Phe Ile Ile Ser 580 585 590		
Lys Cys Asp Thr Val Gly Asp Met Val Gly Thr Leu Val Ser Met Val 595 600 605		
His Ala Thr Gly Ile Pro Ile Val Phe Leu Gly Val Gly Gln His Tyr 610 615 620		

Gly Asp Leu Arg Gly Leu Ser Val Pro Trp Ala Val Asn Leu Leu Met
 625 630 635 640

Lys

<210> 13
 <211> 1564
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 13
 atgcggtggt gcctcactct tctggcattc tgcttcttgg cagttgtacg tgcattaagt 60
 agctccggca gtcgtctgtt ggttggtttg gaagatgcc aagaaaagga attatactcg 120
 aaattatggg ctgacctaga aggtgctcta acctactgaa cttctacgtt aatatgctaa 180
 tattaattgg tagctcgagg atataacctc gacttcgaat cccccaagaa tgacaagctc 240
 agcctgttcg aactcggaga ccgagtctac gaccacatgc ttctcctgcc tcccaagtca 300
 aagggttagc gttaccctta gacatgtcca tatgctctgc tttgtacatc tcaattgacc 360
 tcttggccag gctatggacc ctcccttacc cccaagaata tcattgattt catgaacaag 420
 gacggtaacg tctcctcgc cttgtcgggc aagtccacaa ccgccagcgc tatcagctcg 480
 ctgctattgg agctcgatct ccatctccct gtcgatcggt cctctgtcac cgtcgatcac 540
 ttcaactacg atacactttc tgccctccgat aagcatgatg ttctgtact ccaccgacca 600
 ggcaagttga ggtccgatac caaggctttc tttgatggcg agggcggtgt agcatttccc 660
 agagccgtcc cccacaccct gggcgatgca aacctctca ttgcgcctat tctgcgagcg 720
 cccgccactg cgtatagtta caaccccaag gaggacgcgt cgtcagttga ggatgttgca 780
 gctacgggtt cgcagttggc tctggtctcg gccatgcagg ctagaaactc cgctcggttc 840
 actctactgg gatccgtgga gagtctgcag gatcagtggt tttctgcgac tgtcaaggct 900
 cctggtgatg ggaagcagat gaagacggtc aaccaggaat tcgccaagca gcttactgcg 960
 tggacattca aggaaaccgg agtcctcaag gtcggaaaga tcgagcatca tctggctgaa 1020
 gatggtgaaa tcaactcccg gaagctgaac cctaagatct atcgaataaa gaatgaaact 1080
 gtaagtgaac gccatctgag gttccattgc ctatttgcag gctcaccctt ctcaacaggt 1140
 ctttagcatt gaactttccg aatacaacta tgatcgttac gcgccttcg aggttccaac 1200
 tggcgatgcc gtccagctcg agtttaccat gctgtctccc ttccatcgcc tgaacttgga 1260
 accggtccgt cgaacagata acagtacagt ttacagcaca cgattcacca ccccgatca 1320
 gcatggaatc ttctccttcc gagtgaacta caagcgcccg ttctcaca gaacatgaaga 1380
 aaaacttgag gtgaccgttc gtcatttcgc tcataacgag taaccccgaa gctggaaaat 1440
 cagcggtgga tgggtctgga ttgcgggtct gtggtccgtc atcgctggct tcttagtatt 1500
 cgttgttgca tggctttact cagcgccttc tgccgccgca ctgaacacaa agaagacaca 1560
 ataa 1564

<210> 14
 <211> 1380
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 14
 atgcggtggt gcctcactct tctggcattc tgcttcttgg cagttgtacg tgcattaagt 60
 agctccggca gtcgtctgtt ggttggtttg gaagatgcc aagaaaagga attatactcg 120
 aaattatggg ctgacctaga aggatataac ctgcactcgc aatcccccaa gaatgacaag 180
 ctacgcctgt tcgaactcgg agaccgagtc taccgaccaca tgcttctcct gcctcccaag 240
 tcaaagggtc atggaccctc ccttaccctc aagaatatca ttgatttcat gaacaaggac 300
 ggtaaacgtc tctcgcctt gtcgggcaag tccacaaccg ccagcgctat cagctcgctg 360
 ctattggagc tcgatctcca tctccctgtc gatcggtcct ctgtcaccgt cgatcacttc 420
 aactacgata cactttctgc ctccgataag catgatgttc tgctactcca ccgaccaggc 480
 aagttgaggt ccgataccaa ggctttcttt gatggcgagg gcgtttagc atttcccaga 540
 gccgtcccc acaccctggg cgatgcaaac cctctcattg cgcctattct gcgagcgccc 600
 gccactgcgt atagttacaa cccaaggag gacgcgtcgt cagttgagga tgttgcagct 660

```

acgggttcgc agttggctct ggtctcggcc atgcaggcta gaaactccgc tcggttcact 720
ctactgggat ccgtggagag tctgcaggat cagtggtttt ctgcgactgt caaggctcct 780
ggtgatggga agcagatgaa gacggtcaac caggaattcg ccaagcagct tactgcgtgg 840
acattcaagg aaaccggagt cctcaaggtc ggaaagatcg agcatcatct ggctgaagat 900
ggtgaaatca ctcccagaaa gctgaaccct aagatctatc gaataaagaa tgaaactgtc 960
tttagcattg aactttccga atacaactat gatcgttacg cgcccttcga ggttccaact 1020
ggcgatgccg tccagctcga gtttaccatg ctgtctccct tccatcgctt gaacttggaa 1080
cccgtccgtc gaacagataa cagtacagtt tacagcacac gattcaccac ccccgatcag 1140
catggaatct tctccttccg agtgaactac aagcgcccgt tcctcacgaa catcgaagaa 1200
aaacttgagg tgaccgttcg tcatttcgct cataacgagt acccccgaaag ctggaaaatc 1260
agcggtggat ggggtctggat tgcgggtctg tgggtccgtc tcgctggctt cttagtattc 1320
gttggttgcg ggcctttactc agcgccctct gccgccgcac tgaacacaaa gaagacacaa 1380

```

<210> 15

<211> 460

<212> PRT

<213> *Aspergillus fumigatus*

<400> 15

```

Met Arg Trp Cys Leu Thr Leu Leu Ala Phe Cys Phe Leu Ala Val Val
  1              5              10              15

```

```

Arg Ala Leu Ser Ser Ser Gly Ser Arg Leu Leu Val Val Leu Glu Asp
      20              25              30

```

```

Ala Thr Glu Lys Glu Leu Tyr Ser Lys Leu Trp Ala Asp Leu Glu Gly
      35              40              45

```

```

Tyr Asn Leu Asp Phe Glu Ser Pro Lys Asn Asp Lys Leu Ser Leu Phe
      50              55              60

```

```

Glu Leu Gly Asp Arg Val Tyr Asp His Met Leu Leu Leu Pro Pro Lys
      65              70              75              80

```

```

Ser Lys Gly Tyr Gly Pro Ser Leu Thr Pro Lys Asn Ile Ile Asp Phe
      85              90              95

```

```

Met Asn Lys Asp Gly Asn Val Leu Leu Ala Leu Ser Gly Lys Ser Thr
      100              105              110

```

```

Thr Ala Ser Ala Ile Ser Ser Leu Leu Leu Glu Leu Asp Leu His Leu
      115              120              125

```

```

Pro Val Asp Arg Ser Ser Val Thr Val Asp His Phe Asn Tyr Asp Thr
      130              135              140

```

```

Leu Ser Ala Ser Asp Lys His Asp Val Leu Leu Leu His Arg Pro Gly
      145              150              155              160

```

```

Lys Leu Arg Ser Asp Thr Lys Ala Phe Phe Asp Gly Glu Gly Val Val
      165              170              175

```

```

Ala Phe Pro Arg Ala Val Pro His Thr Leu Gly Asp Ala Asn Pro Leu
      180              185              190

```

```

Ile Ala Pro Ile Leu Arg Ala Pro Ala Thr Ala Tyr Ser Tyr Asn Pro
      195              200              205

```

```

Lys Glu Asp Ala Ser Ser Val Glu Asp Val Ala Ala Thr Gly Ser Gln
      210              215              220

```

Leu Ala Leu Val Ser Ala Met Gln Ala Arg Asn Ser Ala Arg Phe Thr
 225 230 235 240
 Leu Leu Gly Ser Val Glu Ser Leu Gln Asp Gln Trp Phe Ser Ala Thr
 245 250 255
 Val Lys Ala Pro Gly Asp Gly Lys Gln Met Lys Thr Val Asn Gln Glu
 260 265 270
 Phe Ala Lys Gln Leu Thr Ala Trp Thr Phe Lys Glu Thr Gly Val Leu
 275 280 285
 Lys Val Gly Lys Ile Glu His His Leu Ala Glu Asp Gly Glu Ile Thr
 290 295 300
 Pro Glu Lys Leu Asn Pro Lys Ile Tyr Arg Ile Lys Asn Glu Thr Val
 305 310 315 320
 Phe Ser Ile Glu Leu Ser Glu Tyr Asn Tyr Asp Arg Tyr Ala Pro Phe
 325 330 335
 Glu Val Pro Thr Gly Asp Ala Val Gln Leu Glu Phe Thr Met Leu Ser
 340 345 350
 Pro Phe His Arg Leu Asn Leu Glu Pro Val Arg Arg Thr Asp Asn Ser
 355 360 365
 Thr Val Tyr Ser Thr Arg Phe Thr Thr Pro Asp Gln His Gly Ile Phe
 370 375 380
 Ser Phe Arg Val Asn Tyr Lys Arg Pro Phe Leu Thr Asn Ile Glu Glu
 385 390 395 400
 Lys Leu Glu Val Thr Val Arg His Phe Ala His Asn Glu Tyr Pro Arg
 405 410 415
 Ser Trp Lys Ile Ser Gly Gly Trp Val Trp Ile Ala Gly Leu Trp Ser
 420 425 430
 Val Ile Ala Gly Phe Leu Val Phe Val Val Ala Trp Leu Tyr Ser Ala
 435 440 445
 Pro Ser Ala Ala Ala Leu Asn Thr Lys Lys Thr Gln
 450 455 460

<210> 16

<211> 2376

<212> DNA

<213> *Aspergillus fumigatus*

<400> 16

atgtctcagt atcagcttac tgtggccacc agggccaatc agccctatgt acttcctgtc 60
 ctactggtcg caacttccat caacgaggca cgaccaagcc cagtgatatc gatcacctat 120
 gaggatactg cggttcttcg tgaaggagac aaggccgtcg tgcaatacac tggagctagc 180
 ggtaatccta tctttggcct tatcaatgct gttcaggaac tccgcaaaga cttccccttc 240
 cttaacagca aggatgagaa gctggtaaga ggcgccatgg agccttactg ctgatgagca 300
 ctgataagtg atactaacc tccttttata ggagaatgaa tggctgtctc agttggaagc 360
 atttgctcct ctagatttca aggcccttga ccctgaattg cagcgcctcg ataccacact 420

cctgctgaga	tctttcgtcg	tccgttacgc	tctctcgacg	gccgacattg	ccctttgggg	480
tgccatccga	ggcaaccgtg	tccgagttgc	cgcgatcaag	aagggtcac	ttgtcaatgt	540
gactcgttgg	ttctatttct	tggaggatct	gtgcccgtgg	gccacatcta	cactggaggt	600
cttgaaccag	gctgtgagag	agaagaaggc	cgccaaggcg	aaggaggag	ctagctacga	660
catcgctctt	ctcaacactg	aaaaaggcgt	ggtgacaagg	tttcctccc	agccttcagg	720
ttatcttcac	atcggtcacg	caaaagctgc	gctgctcaac	gactactttg	cccacgagaa	780
gtataatggc	acccttcttg	tccgctttga	cgacacaaat	ccttcgaacg	agaagctcga	840
gttccaggac	gcgatcattg	aagatcttgc	tctcatgggc	atcaagccc	acaagatgag	900
ctacaccagt	gactactttg	acgagcttta	ccagtacgcc	cttcaaata	tcaaggacgg	960
taacgcctac	gccgacgata	cagagaagga	ggatcatggc	gagcagagaa	tgaatggaaa	1020
accagcaag	cgtcgtgatg	ccgcgctcga	ggagaacctt	gcccgttcg	aggagatgaa	1080
gaagggtacc	cctgagggtc	tccgttggtg	tatccgagcc	aagatgtctg	tcgataaccc	1140
caacaaggcc	atgctgatc	ctgtcattta	ccgctgcaac	cctgcccctc	accaccgcac	1200
tgggacgaag	tggaagatct	atcctaccta	tgacttcgcc	tgccctatcg	tcgattcaat	1260
tgagggtgtg	actcatgccc	tcagaacccat	tgaataccgc	gatcgcaacc	ctcagtacca	1320
gtgggttctt	gacacgctca	agcttcgcca	tgtccaaatc	tgggattttg	ctcgcatgaa	1380
cttcattcgc	accttgctgt	ctaagagaaa	acttaccagg	ctcgtaacc	aagggtgcgt	1440
ctggggatgg	gatgagtaag	tttacctttg	cttgcaaacg	gattcttgtc	ttactaacga	1500
tgtcagtcct	cgtttcccca	ccatccgagt	aagtaacatg	cctagtcatg	cctgcgaatc	1560
cccttattca	tccggcattt	tttaccatct	cacctacttc	ccatgtactg	ttacttccc	1620
acgctaatac	tttcataggg	catccgacga	aggggaatga	ctatccctgc	tctgagagaa	1680
ttcattctta	agcagggacc	cagcaagaac	atcaccaacc	ttgactggac	cctgatctgg	1740
gcgaccaaca	agaagtacat	tgatcctgtc	gcacctcgtc	acactgccat	tctcaagaag	1800
gatatgggtca	aggcgatcgt	caaggagggc	ccggctacac	cttacacgga	agagaaacct	1860
aagcacggca	agaaccctgc	agttgggtatg	aagaagggtg	tttttggtaa	cacggtcatt	1920
ttcgaccaga	aagatgccaa	gagcttcaag	caagatgaag	agatcacctt	gatgagctgg	1980
ggtaatgcc	ttgtccgtaa	gatcgagacc	gacctacct	caggcatcgt	caaggagctg	2040
gagctggagc	tccacctgga	aggtgacttc	aaaaagaccg	agaagaagg	cacgtggctc	2100
tctactgagg	gacaggacct	aattcccgtt	gaattgggtc	atttcgacta	tctcctcaac	2160
aaggacaccc	tgcaggagga	cgacgtcctt	gaggatgtcc	tgaacaagaa	caccgagttc	2220
agagaggacg	ctgttgctga	ctgcaacgtc	gctgaactga	aagaagggtg	catcatccag	2280
tttgagcgca	agggtctatta	ccgtgttgac	cgggcctatg	taccgggcaa	gccggctgtt	2340
ttgttcaaca	ttcccacggg	caagacgggc	aaatag			2376

<210> 17

<211> 2145

<212> DNA

<213> *Aspergillus fumigatus*

<400> 17

atgtctcagt	atcagcttac	tgtggccacc	agggccaatc	agccctatgt	acttcctgtc	60
ctactgggtc	caacttccat	caacgaggca	cgaccaagcc	cagtgatatc	gatcacctat	120
gaggatactg	cgttcttcg	tgaaggagac	aaggccgtcg	tgcaatacac	tggagctagc	180
ggtaatccta	tctttggcct	tatcaatgct	gttcagggaac	tccgcaaaga	cttccccttc	240
cttaacagca	aggatgagaa	gctggagaat	gaatggctgt	ctcagttgga	agcatttgct	300
cctctagatt	tcaaggccct	tgaccctgaa	ttgcagcgcc	tcgataccca	cctcctgctg	360
agatctttcg	tcgtcgggtta	cgctctctcg	acggccgaca	ttgccctttg	gggtgccatc	420
cgaggcaacc	gtgtcgcagt	tgccgcgac	aagaagggtc	cacttgtcaa	tgtgactcgt	480
tggttctatt	tcttgaggga	tctgtgccc	tgggccacat	ctacactgga	ggtcttgaac	540
caggctgtgc	gagagaagaa	ggccgccaa	gcgaaggagg	gagctagcta	cgacatcgct	600
cttctcaaca	ctgaaaaagg	cgtggtgaca	aggtttcctc	ccgagccttc	aggttatctt	660
cacatcggtc	acgcaaaagc	tgcgctgtc	aacgactact	ttgcccacga	gaagtataat	720
ggcacccttc	ttgtccgctt	tgacgacaca	aatccttcga	acgagaagct	cgagttccag	780
gacgcgatca	ttgaagatct	tgtctcatg	ggcatcaagc	ccgacaagat	gagctacacc	840
agtgactact	ttgacgagct	ttaccagtac	gcccttcaaa	tcatacaagga	cggtaacgcc	900
tacgccgacg	ataccgagaa	ggagggtcatg	gctgagcaga	gaatgaatgg	aaaaccagc	960
aagcgtcgtg	atgcatccgt	cgaggagaa	cttgcccgtc	tcgaggagat	gaagaagggt	1020
acccttgagg	gtctccggtt	gtgtatccga	gccaagatgt	ctgtcgataa	ccccaaaca	1080
gccatgcgtg	atcctgtcat	ttaccgtgc	aaccctgccc	ctcaccaccg	cactgggacg	1140
aagtgaagaa	tctatcctac	ctatgacttc	gcctgccta	tcgtcgattc	aattgagggt	1200

```

gtgactcatg ccctcagaac cattgaatac cgcgatcgca accctcagta ccagtgggtc 1260
ttggacacgc tcaagcttcg ccatgtccaa atctgggatt ttgctcgcat gaacttcatt 1320
cgcaccttgc tgtctaagag aaaacttacc aagctcgta accaaggtgt cgtctgggga 1380
tgggatgata ctcgtttccc caccatccga ggcacccgac gaaggggaat gactatccct 1440
gctctgagag aattcattct taagcaggga cccagcaaga acatcaccaa ccttgactgg 1500
accctgatct gggcgaccaa caagaagtac attgatcctg tcgcacctcg tcacactgcc 1560
attctcaaga aggatatggt caaggcgatc gtcaaggagg gcccgggtac accttacacg 1620
gaagagaaac ctaagcacgg caagaaccct gcagttggta tgaagaaggt ggtttttggg 1680
aacacgggtca ttttcgacca gaaagatgcc aagagcttca agcaagatga agagatcacc 1740
ttgatgagct ggggtaatgc cattgtccgt aagatcgaga ccgatacctac ctcaggcatc 1800
gtcaaggagc tggagctgga gctccacctg gaaggtgact tcaaaaagac cgagaagaag 1860
gtcacgtggc tctctactga gggacaggac ctaattcccc ttgaattggg cgatttcgac 1920
tatctcctca acaaggacac cctgcaggag gacgacgtcc ttgaggatgt cctgaacaag 1980
aacaccgagt tcagagagga cgctgttgct gactgcaacg tcgctgaact gaaagaaggt 2040
gacatcatcc agtttgagcg caagggtat taccgtgtg accgggccta tgtaccgggc 2100
aagccggctg ttttgttcaa cattcccacg ggcaagacgg gcaaa 2145

```

<210> 18

<211> 715

<212> PRT

<213> *Aspergillus fumigatus*

<400> 18

```

Met Ser Gln Tyr Gln Leu Thr Val Ala Thr Arg Ala Asn Gln Pro Tyr
  1              5              10              15

```

```

Val Leu Pro Val Leu Leu Val Ala Thr Ser Ile Asn Glu Ala Arg Pro
      20              25              30

```

```

Ser Pro Val Ile Ser Ile Thr Tyr Glu Asp Thr Ala Val Leu Arg Glu
      35              40              45

```

```

Gly Asp Lys Ala Val Val Gln Tyr Thr Gly Ala Ser Gly Asn Pro Ile
      50              55              60

```

```

Phe Gly Leu Ile Asn Ala Val Gln Glu Leu Arg Lys Asp Phe Pro Phe
      65              70              75              80

```

```

Leu Asn Ser Lys Asp Glu Lys Leu Glu Asn Glu Trp Leu Ser Gln Leu
      85              90              95

```

```

Glu Ala Phe Ala Pro Leu Asp Phe Lys Ala Leu Asp Pro Glu Leu Gln
      100             105             110

```

```

Arg Leu Asp Thr His Leu Leu Leu Arg Ser Phe Val Val Gly Tyr Ala
      115             120             125

```

```

Leu Ser Thr Ala Asp Ile Ala Leu Trp Gly Ala Ile Arg Gly Asn Arg
      130             135             140

```

```

Val Ala Val Ala Ala Ile Lys Lys Gly Ser Leu Val Asn Val Thr Arg
      145             150             155             160

```

```

Trp Phe Tyr Phe Leu Glu Asp Leu Cys Pro Trp Ala Thr Ser Thr Leu
      165             170             175

```

```

Glu Val Leu Asn Gln Ala Val Arg Glu Lys Lys Ala Ala Lys Ala Lys
      180             185             190

```

```

Glu Gly Ala Ser Tyr Asp Ile Ala Leu Leu Asn Thr Glu Lys Gly Val

```

195					200					205					
Val	Thr	Arg	Phe	Pro	Pro	Glu	Pro	Ser	Gly	Tyr	Leu	His	Ile	Gly	His
210						215					220				
Ala	Lys	Ala	Ala	Leu	Leu	Asn	Asp	Tyr	Phe	Ala	His	Glu	Lys	Tyr	Asn
225						230					235				240
Gly	Thr	Leu	Leu	Val	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Ser	Asn	Glu	Lys
				245					250					255	
Leu	Glu	Phe	Gln	Asp	Ala	Ile	Ile	Glu	Asp	Leu	Ala	Leu	Met	Gly	Ile
			260					265					270		
Lys	Pro	Asp	Lys	Met	Ser	Tyr	Thr	Ser	Asp	Tyr	Phe	Asp	Glu	Leu	Tyr
		275					280					285			
Gln	Tyr	Ala	Leu	Gln	Ile	Ile	Lys	Asp	Gly	Asn	Ala	Tyr	Ala	Asp	Asp
	290					295					300				
Thr	Glu	Lys	Glu	Val	Met	Ala	Glu	Gln	Arg	Met	Asn	Gly	Lys	Pro	Ser
305						310					315				320
Lys	Arg	Arg	Asp	Ala	Ser	Val	Glu	Glu	Asn	Leu	Ala	Arg	Phe	Glu	Glu
				325					330					335	
Met	Lys	Lys	Gly	Thr	Pro	Glu	Gly	Leu	Arg	Trp	Cys	Ile	Arg	Ala	Lys
			340					345					350		
Met	Ser	Val	Asp	Asn	Pro	Asn	Lys	Ala	Met	Arg	Asp	Pro	Val	Ile	Tyr
		355					360					365			
Arg	Cys	Asn	Pro	Ala	Pro	His	His	Arg	Thr	Gly	Thr	Lys	Trp	Lys	Ile
	370					375					380				
Tyr	Pro	Thr	Tyr	Asp	Phe	Ala	Cys	Pro	Ile	Val	Asp	Ser	Ile	Glu	Gly
385						390					395				400
Val	Thr	His	Ala	Leu	Arg	Thr	Ile	Glu	Tyr	Arg	Asp	Arg	Asn	Pro	Gln
				405					410					415	
Tyr	Gln	Trp	Phe	Leu	Asp	Thr	Leu	Lys	Leu	Arg	His	Val	Gln	Ile	Trp
			420					425					430		
Asp	Phe	Ala	Arg	Met	Asn	Phe	Ile	Arg	Thr	Leu	Leu	Ser	Lys	Arg	Lys
		435					440					445			
Leu	Thr	Lys	Leu	Val	Asn	Gln	Gly	Val	Val	Trp	Gly	Trp	Asp	Asp	Pro
	450					455					460				
Arg	Phe	Pro	Thr	Ile	Arg	Gly	Ile	Arg	Arg	Arg	Gly	Met	Thr	Ile	Pro
465						470					475				480
Ala	Leu	Arg	Glu	Phe	Ile	Leu	Lys	Gln	Gly	Pro	Ser	Lys	Asn	Ile	Thr
				485					490					495	
Asn	Leu	Asp	Trp	Thr	Leu	Ile	Trp	Ala	Thr	Asn	Lys	Lys	Tyr	Ile	Asp
			500					505					510		
Pro	Val	Ala	Pro	Arg	His	Thr	Ala	Ile	Leu	Lys	Lys	Asp	Met	Val	Lys
		515					520					525			

Ala Ile Val Lys Gly Gly Pro Ala Thr Pro Tyr Thr Glu Glu Lys Pro
 530 535 540

Lys His Gly Lys Asn Pro Ala Val Gly Met Lys Lys Val Val Phe Gly
 545 550 555 560

Asn Thr Val Ile Phe Asp Gln Lys Asp Ala Lys Ser Phe Lys Gln Asp
 565 570 575

Glu Glu Ile Thr Leu Met Ser Trp Gly Asn Ala Ile Val Arg Lys Ile
 580 585 590

Glu Thr Asp Pro Thr Ser Gly Ile Val Lys Glu Leu Glu Leu Glu Leu
 595 600 605

His Leu Glu Gly Asp Phe Lys Lys Thr Glu Lys Lys Val Thr Trp Leu
 610 615 620

Ser Thr Glu Gly Gln Asp Leu Ile Pro Val Glu Leu Val Asp Phe Asp
 625 630 635 640

Tyr Leu Leu Asn Lys Asp Thr Leu Gln Glu Asp Asp Val Leu Glu Asp
 645 650 655

Val Leu Asn Lys Asn Thr Glu Phe Arg Glu Asp Ala Val Ala Asp Cys
 660 665 670

Asn Val Ala Glu Leu Lys Glu Gly Asp Ile Ile Gln Phe Glu Arg Lys
 675 680 685

Gly Tyr Tyr Arg Val Asp Arg Ala Tyr Val Pro Gly Lys Pro Ala Val
 690 695 700

Leu Phe Asn Ile Pro Thr Gly Lys Thr Gly Lys
 705 710 715

<210> 19

<211> 2639

<212> DNA

<213> *Aspergillus fumigatus*

<400> 19

```

atgtcgccat caatataccta catttcaggc cagcttaggc agctaataata ctatcatctc 60
gataacaatt tgtgccgtaa tgcgctgttc ctgcgccgtc gtttacatgc ttacgagccc 120
cgaacggcgg aagcgtcgta tttactcgct ctctgccatc ttcagaacgg gcaagtcaaa 180
gccgcatacg attacagcag gaattttgga tcgagaggca cccacctcgg ctgctcctat 240
gtcttcgcgc aagcgtgctt ggacctagga aagtatctgg aaggatcac agcgtagag 300
cggagtaaag gcctttgggc ttcgaagaac cactggagta agtattccat gcgctgatac 360
ttgcagtcga cctgcattta tttcgttgct ttctgttact gacacatttc caccttgtgc 420
tctagataag cacagtgaga cgcgaagaca acatctgccg gatgcagccg cagtattctg 480
cctgttaggt aaattatggc atgcgcataa ggacatcaac aaagctgtgg aatgctatgt 540
tgaatctctg aagctgaatc cttcatgtg ggatgcgttc caagggttgt gcgacaccgg 600
taagctttgg agaataaacc taatacatct agccatggct aattgtgttc taccgccaag 660
gagtcaatgt ccgcgtgtca aacatctaca agttgaattc tgaattgctg gccgtattgt 720
cttcatcgcc acaggcggat gctgagccaa tatccgataa gtctgcacac acgaatgggc 780
cactgcaagc gcaggcgaat gttaatccaa gttccgatcc ttttgccctg actacttctc 840
gcagtgattc aggtaccagc catgggagct ctgccttgtg ggaaaaacta aatggaagca 900
cagtaagcgt ggcgtcatcg ggagtgccag catcaatcgt gcatgaagga gccgaaacgc 960

```


cgagtgggtca	aagcagcgga	tctgatgagt	tccggttagc	taacggaatg	aacggcgcg	1020
atgcttcttg	ggaccctcct	ttagctcctg	caaggaaaaa	cagaacgatc	caggcaataa	1080
gcggcgagta	tccaatggac	cctcctccca	agatgaaacc	cactgggatc	cgaccaagga	1140
caaggaccag	gactgagccg	gaggaccaa	tttcagccca	gatagaccgg	gaggcaacaa	1200
atgcgcccag	ggtcggggac	cgaaacgaa	ctgtttctgg	tcaggtagcg	catccaccga	1260
cgtcacaacc	cacagaacca	ggagcacc	agcggcgag	tgtgcgactc	ttcaaccaga	1320
ttaaaccac	gaccagcaaa	ttgtcggcgt	ccgcgctggg	agtcaaggat	gctagagaag	1380
tcaagaaagc	gaaagccaca	ggtacgaagg	ggcgtacgac	aaccaccacc	atgggacgag	1440
tagtgagtgg	cagccgaaaa	catgccagcg	aacatcatga	tgcagatggt	aaagacggag	1500
ggtcgggtacc	gtccgcccac	actcacgcca	tctccaaagg	cgctgctcaa	gaaagatcga	1560
aagaaatcga	ggcgttgacc	tggctgctgg	agctattctc	gaaacttgct	tctggattct	1620
ttgccttggtg	tcgctaccga	tgcccagagt	caatccagat	cttcaattcg	ctctctcaag	1680
gccaacggga	aacaccgtgg	gttctcgctc	agattggacg	agcgtactat	gagcaggcta	1740
tgtattccga	ggcagaaaag	tacttctacc	gtgtgaagac	catggcacc	tcgcgcttg	1800
aagacatgga	gatctactcg	actgtccttt	ggcatctgaa	gaacgatgtt	gagttagcct	1860
atttggcgca	tgagttgatg	gaaacagacc	gcctgtcgcc	acaggcggtg	tgccgcatcg	1920
gtaattcggt	ttcccaccag	cgagatcatg	accaggcctt	gaagtgcctt	aagcgggcaa	1980
cccagctgga	tcctcagttt	gcctacgggt	ttactcttca	agggcacgag	tatgttgcca	2040
acgaagaata	cgacaaggcg	cttcatgcat	accgtcacgg	tatcagcgcg	gatagtcggc	2100
attacaatgc	ttggtacgga	ctgggcacgg	tttatgacaa	aatgggcaaa	ctggactttg	2160
ccgaacaaca	cttcgggaat	gcggcaagca	ttaaccgac	caacgcagtt	ttgatctgct	2220
gcattggatt	ggtactggaa	aaaatgaaca	accctaaagc	ggctctcggt	caatatggtc	2280
gcgcttggtc	cttggcacct	cattccgtac	tcgcgcgatt	ccgcaaggcc	cgcgattga	2340
tgaagctcca	ggagctcaaa	ttagctctgt	ctgagttgaa	gattctcaaa	gacatggctc	2400
cagacgaagc	taacgtgcat	tatctgttgg	gtaagctcta	caaaatgctt	cacgacaaag	2460
ccaatgccat	taagcacttc	acaactgctt	tgaacttgga	tccaaaggta	tgccatcac	2520
ttccattccg	tcaaatattc	agacaatact	aacggattcg	gttacaggca	gcacaataca	2580
tcaaggatgc	catggaatct	cttgacgatg	acgaggagga	tgatgaggac	atgagctga	2639

<210> 20

<211> 2427

<212> DNA

<213> *Aspergillus fumigatus*

<400> 20

atgtcgccat	caatatccta	catttcaggc	cagcttaggc	agctaataata	ctatcatctc	60
gataacaatt	tgtgccgtaa	tgcgctgttc	ctcgccggtc	gtttacatgc	ttacgagccc	120
cgaacggcgg	aagcgtcgta	tttactcgct	ctctgccatc	ttcagaacgg	gcaagtcaaa	180
gccgcatacg	attacagcag	gaattttgga	tcgagaggca	cccacctcgg	ctgctcctat	240
gtcttcgcgc	aagcgtgctt	ggacctagga	aagtatctgg	aaggatatcac	agcgttagag	300
cggagtaaag	gcctttgggc	ttcgaagaac	cactggaata	agcacagtga	gacgcgaaga	360
caacatctgc	cggatgcagc	cgcagtattc	tgcctgttag	gtaaatattg	gcatgcgcac	420
aaggacatca	acaaagctgt	ggaatgctat	gttgaatctc	tgaagctgaa	tcccttcacg	480
tgggatgcgt	tccaagggtt	gtgcgacacc	ggagctcaatg	tccgcgtgtc	aaacatctac	540
aagtngaatt	ctgaattgct	ggccgtattg	tcttcatcgc	cacaggcgga	tgctgagcca	600
atatccgata	agtctgcaca	cacgaatggg	ccactgcaag	cgcaggcgaa	tgtaaatcca	660
agttccgata	cttttgcttc	gactacttct	cgcagtgatt	caggtaccag	ccatgggagc	720
tctgccttgt	gggaaaaact	aaatggaagc	acagtaagcg	tggcgtcatc	gggagtgcga	780
gcatcaatcg	tgcatgaagg	agccgaaacg	ccgagtggtc	aaagcagcgg	atctgatgag	840
ttccggttag	ctaacggaat	gaacggcgcg	gatgcttctt	gggacctctc	tttagctcct	900
gcaaggaaaa	acagaacgat	ccaggcaata	agcggcgagt	atccaatgga	ccctcctccc	960
aagatgaaac	ccactgggat	ccgaccaagg	acaaggacca	ggactgagcc	ggaggaccaa	1020
atttcagccc	agatagaccg	ggaggcaaca	aatgcgcca	gggtcgggga	ccgcaaacga	1080
actgtttctg	gtcaggtagc	gcatccaccg	acgtcacac	ccacagaacc	aggagcacc	1140
cagcggcgga	gtgtgcgact	cttcaaccag	attaaaccca	cgaccagcaa	attgtcgggc	1200
tccgcgctgg	gagtcaagga	tgctagagaa	gtcaagaaag	cgaaagccac	aggtacgaag	1260
gggcgtacga	caaccaccac	catgggacga	gtagttagtg	gcagccgaaa	acatgccagc	1320
gaacatcatg	atgcagatgg	taaagacgga	cggctcggtac	cgtccgcca	cactcacgcc	1380
atctccaaag	gcgctgctca	agaaagatcg	aaagaaatcg	aggcgttgac	ctggctgctg	1440
gagctattct	cgaaacttgc	ttctggattc	tttgccttgt	gtcgtctaccg	atgcccagag	1500

```

tcaatccaga tcttcaattc gctctctcaa ggccaacggg aaacaccgtg ggttctcgct 1560
cagattggac gagcgtaacta tgagcaggct atgtattccg aggcagaaaa gtacttctac 1620
cgtgtgaaga ccatggcacc ctgcgcgttg gaagacatgg agatctactc gactgtcctt 1680
tggtcatctga agaacgatgt tgagttagcc tatttggcgc atgagttgat ggaaacagac 1740
cgcctgtcgc cacaggcgtg gtgcgccatc ggtaattcgt tttcccacca gcgagatcat 1800
gaccaggcct tgaagtgctt taagcgggca acccagctgg atcctcagtt tgcctacggg 1860
tttactcttc aagggcacga gtatgttgcc aacgaagaat acgacaaggc gcttgatgca 1920
taccgtcacg gtatcagcgc ggatagtcgg cattacaatg cttggtacgg actgggcacg 1980
gtttatgaca aaatgggcaa actggacttt gccgaacaac acttccggaa tgcggcaagc 2040
attaacccga ccaacgcagt tttgatctgc tgcattggat tggtagctga aaaaatgaac 2100
aaccctaaag cggctctcgt gcaatatggt cgcgcttggt ccttggcacc tcattccgta 2160
ctcgcgcgat tccgcaaggc ccgcgcattg atgaagctcc aggagctcaa attagctctg 2220
tctgagttga agattctcaa agacatggct ccagacgaag ctaacgtgca ttatctgttg 2280
ggtaagctct acaaaatgct tcacgacaaa gccaatgcca ttaagcactt cacaactgct 2340
ttgaacttgg atccaaaggc agcacaatac atcaaggatg ccatggaatc tcttgacgat 2400
gacgaggagg atgatgagga catgagc 2427

```

<210> 21

<211> 809

<212> PRT

<213> *Aspergillus fumigatus*

<400> 21

```

Met Ser Pro Ser Ile Ser Tyr Ile Ser Gly Gln Leu Arg Gln Leu Ile
  1              5              10              15

Tyr Tyr His Leu Asp Asn Asn Leu Cys Arg Asn Ala Leu Phe Leu Ala
      20              25              30

Gly Arg Leu His Ala Tyr Glu Pro Arg Thr Ala Glu Ala Ser Tyr Leu
      35              40              45

Leu Ala Leu Cys His Leu Gln Asn Gly Gln Val Lys Ala Ala Tyr Asp
      50              55              60

Tyr Ser Arg Asn Phe Gly Ser Arg Gly Thr His Leu Gly Cys Ser Tyr
      65              70              75              80

Val Phe Ala Gln Ala Cys Leu Asp Leu Gly Lys Tyr Leu Glu Gly Ile
      85              90              95

Thr Ala Leu Glu Arg Ser Lys Gly Leu Trp Ala Ser Lys Asn His Trp
      100             105             110

Asn Lys His Ser Glu Thr Arg Arg Gln His Leu Pro Asp Ala Ala Ala
      115             120             125

Val Phe Cys Leu Leu Gly Lys Leu Trp His Ala His Lys Asp Ile Asn
      130             135             140

Lys Ala Val Glu Cys Tyr Val Glu Ser Leu Lys Leu Asn Pro Phe Met
      145             150             155             160

Trp Asp Ala Phe Gln Gly Leu Cys Asp Thr Gly Val Asn Val Arg Val
      165             170             175

Ser Asn Ile Tyr Lys Leu Asn Ser Glu Leu Leu Ala Val Leu Ser Ser
      180             185             190

Ser Pro Gln Ala Asp Ala Glu Pro Ile Ser Asp Lys Ser Ala His Thr

```

195					200					205					
Asn	Gly	Pro	Leu	Gln	Ala	Gln	Ala	Asn	Val	Asn	Pro	Ser	Ser	Asp	Pro
210					215					220					
Phe	Ala	Ser	Thr	Thr	Ser	Arg	Ser	Asp	Ser	Gly	Thr	Ser	His	Gly	Ser
225					230					235					240
Ser	Ala	Leu	Trp	Glu	Lys	Leu	Asn	Gly	Ser	Thr	Val	Ser	Val	Ala	Ser
				245					250					255	
Ser	Gly	Val	Pro	Ala	Ser	Ile	Val	His	Glu	Gly	Ala	Glu	Thr	Pro	Ser
			260					265					270		
Gly	Gln	Ser	Ser	Gly	Ser	Asp	Glu	Phe	Arg	Leu	Ala	Asn	Gly	Met	Asn
		275					280					285			
Gly	Ala	Asp	Ala	Ser	Trp	Asp	Pro	Pro	Leu	Ala	Pro	Ala	Arg	Lys	Asn
	290					295					300				
Arg	Thr	Ile	Gln	Ala	Ile	Ser	Gly	Glu	Tyr	Pro	Met	Asp	Pro	Pro	Pro
305					310					315					320
Lys	Met	Lys	Pro	Thr	Gly	Ile	Arg	Pro	Arg	Thr	Arg	Thr	Arg	Thr	Glu
				325					330					335	
Pro	Glu	Asp	Gln	Ile	Ser	Ala	Gln	Ile	Asp	Arg	Glu	Ala	Thr	Asn	Ala
			340					345					350		
Pro	Arg	Val	Gly	Asp	Arg	Lys	Arg	Thr	Val	Ser	Gly	Gln	Val	Ala	His
		355					360					365			
Pro	Pro	Thr	Ser	Gln	Pro	Thr	Glu	Pro	Gly	Ala	Pro	Gln	Arg	Arg	Ser
		370				375					380				
Val	Arg	Leu	Phe	Asn	Gln	Ile	Lys	Pro	Thr	Thr	Ser	Lys	Leu	Ser	Ala
385					390					395					400
Ser	Ala	Leu	Gly	Val	Lys	Asp	Ala	Arg	Glu	Val	Lys	Lys	Ala	Lys	Ala
			405						410					415	
Thr	Gly	Thr	Lys	Gly	Arg	Thr	Thr	Thr	Thr	Thr	Met	Gly	Arg	Val	Val
			420					425					430		
Ser	Gly	Ser	Arg	Lys	His	Ala	Ser	Glu	His	His	Asp	Ala	Asp	Gly	Lys
		435					440					445			
Asp	Gly	Arg	Ser	Val	Pro	Ser	Ala	His	Thr	His	Ala	Ile	Ser	Lys	Gly
	450					455					460				
Ala	Ala	Gln	Glu	Arg	Ser	Lys	Glu	Ile	Glu	Ala	Leu	Thr	Trp	Leu	Leu
465					470					475					480
Glu	Leu	Phe	Ser	Lys	Leu	Ala	Ser	Gly	Phe	Phe	Ala	Leu	Cys	Arg	Tyr
			485						490					495	
Arg	Cys	Pro	Glu	Ser	Ile	Gln	Ile	Phe	Asn	Ser	Leu	Ser	Gln	Gly	Gln
		500						505					510		
Arg	Glu	Thr	Pro	Trp	Val	Leu	Ala	Gln	Ile	Gly	Arg	Ala	Tyr	Tyr	Glu
		515					520					525			

Gln Ala Met Tyr Ser Glu Ala Glu Lys Tyr Phe Tyr Arg Val Lys Thr
 530 535 540
 Met Ala Pro Ser Arg Leu Glu Asp Met Glu Ile Tyr Ser Thr Val Leu
 545 550 555 560
 Trp His Leu Lys Asn Asp Val Glu Leu Ala Tyr Leu Ala His Glu Leu
 565 570 575
 Met Glu Thr Asp Arg Leu Ser Pro Gln Ala Trp Cys Ala Ile Gly Asn
 580 585 590
 Ser Phe Ser His Gln Arg Asp His Asp Gln Ala Leu Lys Cys Phe Lys
 595 600 605
 Arg Ala Thr Gln Leu Asp Pro Gln Phe Ala Tyr Gly Phe Thr Leu Gln
 610 615 620
 Gly His Glu Tyr Val Ala Asn Glu Glu Tyr Asp Lys Ala Leu Asp Ala
 625 630 635 640
 Tyr Arg His Gly Ile Ser Ala Asp Ser Arg His Tyr Asn Ala Trp Tyr
 645 650 655
 Gly Leu Gly Thr Val Tyr Asp Lys Met Gly Lys Leu Asp Phe Ala Glu
 660 665 670
 Gln His Phe Arg Asn Ala Ala Ser Ile Asn Pro Thr Asn Ala Val Leu
 675 680 685
 Ile Cys Cys Ile Gly Leu Val Leu Glu Lys Met Asn Asn Pro Lys Ala
 690 695 700
 Ala Leu Val Gln Tyr Gly Arg Ala Cys Ser Leu Ala Pro His Ser Val
 705 710 715 720
 Leu Ala Arg Phe Arg Lys Ala Arg Ala Leu Met Lys Leu Gln Glu Leu
 725 730 735
 Lys Leu Ala Leu Ser Glu Leu Lys Ile Leu Lys Asp Met Ala Pro Asp
 740 745 750
 Glu Ala Asn Val His Tyr Leu Leu Gly Lys Leu Tyr Lys Met Leu His
 755 760 765
 Asp Lys Ala Asn Ala Ile Lys His Phe Thr Thr Ala Leu Asn Leu Asp
 770 775 780
 Pro Lys Ala Ala Gln Tyr Ile Lys Asp Ala Met Glu Ser Leu Asp Asp
 785 790 795 800
 Asp Glu Glu Asp Asp Glu Asp Met Ser
 805

<210> 22

<211> 1836

<212> DNA

<213> *Aspergillus fumigatus*

<400> 22

```

gcccactacg gtttacaatc gggaattccc gatgaggtgg actttgcatt gtatcacctt 60
gttcagattt cgaatcaacg atgggataaa ttcaagtttg agggtttccc cttgcttgcg 120
gagaacctca tggcaaaggc cctggatata tcccttgatc caaccggggt gaagtgggag 180
cttcagtatg atgttcttca actcagtgat cgcgtcaatg agctgaactc gctacatggc 240
acacgagatc tgttgagaaa gatcaaacaa atgccagtta cattgccgga agacaccctc 300
gagacgtacg aattcaacca ccttctgcgc aacgttaaag aagcgaccct ggtactacgc 360
aatatgggtcc ttctgaaaga gaatgcctac tatgtgtcac ggtacgcgaa aggcctgctc 420
cgagacttcc tcgtcattat gatcaacttg cccaatcagc ctcgtctcaa cgagatcaag 480
aacgacgctt tggacattgc agaggaggtc accaagttaa tgaagaccga tccggaagat 540
ccactttgga tctcacttct caattgtctc gggtcgtcag atcgtgctca cgtgggtccgc 600
gcactctggg ctctcaccca tttctccact gaattagacg agccagaggc gaaccgggca 660
atggaacgga taccaaaaga gactttgcag cagctctact ttcacactct tctcgacttg 720
gacaaagata ttctcagtggt tgcattggac ttctgggtacc agtatacact ttcgtccgag 780
aacattgaga ctttgattga ggtcttcaac ttgcctaccg tcttcgtccc ccggatgggtc 840
gcactgttaa cgcacgaagg ccgaccgaac aagaaggaaa ctgtgttgca agaagaaaag 900
gtggccccc caccgtcggg tatccctcgt gtaccgccc agctcatgaa agagctgatg 960
gagctttcgg agcctgaacg gagctcgcgt tggctccggg gctgctttgt ggaggacctc 1020
gagtgcgaga tcacccaaat tgccttgtgg caggcgtatc agagcagatt tgcagaccct 1080
cgccttctctg gtggcgggtgt tctccctgcg gctgaattta tcaaaaatgt cagtacgact 1140
ttcacgaacg cgcaagcaca ggtgatcaat ggccctgggtg cagccacgaa attcatcatc 1200
aaaggcattc ggccctgga gaccgcctat accttcgagg gctttcccta catttactgc 1260
aagtgggagg acaactcgaa gccaaagcaag acgtgtcagc gtgctttcaa gtcgcccggca 1320
gaacttcgcc atcacgtctt cacggaacac atgaacctca agcctactga aacgccggga 1380
cactataacc tggagaaggc ggagtcgccc gttcatacct gcctttggga caactgcacg 1440
aaattccggt cgtctggtcc gagtgcctat actgcaatgg tcgtgggca cgtctccgca 1500
catctgccc aggaacgtgc gccagatgag gagccgcga catccaaacg tgcggttctc 1560
caagagcgca tcgtccgcaa atggtactac ttggcactc cagtcaatga gcgaggcgag 1620
ccgtttggag tggcctacaa ggcgcggtta gtattgcgta acctgcccg aaacctgcct 1680
acgggtattg caccgcagta caacgggctt tcatggaaga aagccgtctt ccttagtcat 1740
cgtccaaaga tcacgaagc atgggaccgc aaccgctcat tgcgcaagga acttaccgag 1800
ttgatcatgg taatagaaaa agaggattat tactga 1836

```

<210> 23

<211> 1836

<212> DNA

<213> *Aspergillus fumigatus*

<400> 23

```

gcccactacg gtttacaatc gggaattccc gatgaggtgg actttgcatt gtatcacctt 60
gttcagattt cgaatcaacg atgggataaa ttcaagtttg agggtttccc cttgcttgcg 120
gagaacctca tggcaaaggc cctggatata tcccttgatc caaccggggt gaagtgggag 180
cttcagtatg atgttcttca actcagtgat cgcgtcaatg agctgaactc gctacatggc 240
acacgagatc tgttgagaaa gatcaaacaa atgccagtta cattgccgga agacaccctc 300
gagacgtacg aattcaacca ccttctgcgc aacgttaaag aagcgaccct ggtactacgc 360
aatatgggtcc ttctgaaaga gaatgcctac tatgtgtcac ggtacgcgaa aggcctgctc 420
cgagacttcc tcgtcattat gatcaacttg cccaatcagc ctcgtctcaa cgagatcaag 480
aacgacgctt tggacattgc agaggaggtc accaagttaa tgaagaccga tccggaagat 540
ccactttgga tctcacttct caattgtctc gggtcgtcag atcgtgctca cgtgggtccgc 600
gcactctggg ctctcaccca tttctccact gaattagacg agccagaggc gaaccgggca 660
atggaacgga taccaaaaga gactttgcag cagctctact ttcacactct tctcgacttg 720
gacaaagata ttctcagtggt tgcattggac ttctgggtacc agtatacact ttcgtccgag 780
aacattgaga ctttgattga ggtcttcaac ttgcctaccg tcttcgtccc ccggatgggtc 840
gcactgttaa cgcacgaagg ccgaccgaac aagaaggaaa ctgtgttgca agaagaaaag 900
gtggccccc caccgtcggg tatccctcgt gtaccgccc agctcatgaa agagctgatg 960
gagctttcgg agcctgaacg gagctcgcgt tggctccggg gctgctttgt ggaggacctc 1020
gagtgcgaga tcacccaaat tgccttgtgg caggcgtatc agagcagatt tgcagaccct 1080
cgccttctctg gtggcgggtgt tctccctgcg gctgaattta tcaaaaatgt cagtacgact 1140
ttcacgaacg cgcaagcaca ggtgatcaat ggccctgggtg cagccacgaa attcatcatc 1200

```

```

aaaggcattc ggcccctgga gaccgcctat accttcgagg gctttcccta catttactgc 1260
aagtgggchg acaactcgaa gccaagcaag acgtgtcagc gtgctttcaa gtcgcccggca 1320
gaacttcgcc atcacgtctt cacggaacac atgaacctca agcctactga aacgccggga 1380
cactataacc tggagaaggc ggagtcgccc gttcatacct gcctttggga caactgcacg 1440
aaattccggt cgtctggtcc gagtgccaat actgcaatgg tcgctgggca cgtctccgca 1500
catctgcccg aggaacgtgc gccagatgcg gagccgccga catccaaacg tgcggttctc 1560
caagagcgca tcgtccgcaa atggtactac ctggacactc cagtcaatga gcgagggcgag 1620
ccgtttggag tggcctacaa ggcggcgtta gtattgcgta accttgcccg aaacctgcct 1680
acgggtattg caccgcagta caacgggctt tcatggaaga aagccgtctt ccttagtcat 1740
cgtccaaaga tcatcgaagc atgggaccgc aaccgctcat tgcgcaagga acttaccgag 1800
ttgatcatgg taatagaaaa agaggattat tactga 1836

```

<210> 24

<211> 611

<212> PRT

<213> *Aspergillus fumigatus*

<400> 24

```

Ala His Tyr Gly Leu Gln Ser Gly Ile Pro Asp Glu Val Asp Phe Ala
  1              5              10              15

```

```

Leu Tyr His Leu Val Gln Ile Ser Asn Gln Arg Trp Asp Lys Phe Lys
          20              25              30

```

```

Phe Glu Gly Phe Pro Leu Leu Ala Glu Asn Leu Met Ala Lys Ala Leu
      35              40              45

```

```

Asp Ile Ser Leu Val Thr Thr Gly Val Lys Trp Glu Leu Gln Tyr Asp
      50              55              60

```

```

Val Leu Gln Leu Ser Asp Arg Val Asn Glu Leu Asn Ser Leu His Gly
      65              70              75              80

```

```

Thr Arg Asp Leu Leu Glu Lys Ile Lys Gln Met Pro Val Thr Leu Pro
          85              90              95

```

```

Glu Asp Thr Leu Glu Thr Tyr Glu Phe Asn His Leu Leu Arg Asn Val
      100              105              110

```

```

Lys Glu Ala Thr Leu Val Leu Arg Asn Met Val Leu Leu Lys Glu Asn
      115              120              125

```

```

Ala Tyr Tyr Val Ser Arg Tyr Ala Lys Gly Leu Leu Arg Asp Phe Leu
      130              135              140

```

```

Val Ile Met Ile Asn Leu Pro Asn Gln Pro Arg Leu Asn Glu Ile Lys
      145              150              155              160

```

```

Asn Asp Ala Leu Asp Ile Ala Glu Glu Val Thr Lys Phe Met Lys Thr
          165              170              175

```

```

Asp Pro Glu Asp Pro Leu Trp Ile Ser Leu Leu Asn Cys Leu Gly Ser
          180              185              190

```

```

Ser Asp Arg Ala His Val Val Arg Ala Leu Trp Ala Leu Thr His Phe
      195              200              205

```

```

Ser Thr Glu Leu Asp Glu Pro Glu Ala Asn Arg Ala Met Glu Arg Ile
      210              215              220

```

Pro Lys Glu Thr Leu Gln Gln Leu Tyr Phe His Thr Leu Leu Asp Leu
 225 230 235 240
 Asp Lys Asp Ile Leu Ser Gly Ala Leu Asp Phe Trp Tyr Gln Tyr Thr
 245 250 255
 Leu Ser Ser Glu Asn Ile Glu Thr Leu Ile Glu Val Phe Asn Leu Pro
 260 265 270
 Thr Val Phe Val Pro Arg Met Val Ala Leu Leu Thr His Glu Gly Arg
 275 280 285
 Pro Asn Lys Lys Glu Thr Val Leu Gln Glu Glu Lys Val Ala Pro Pro
 290 295 300
 Pro Ser Asp Ile Pro Arg Val Pro Pro Glu Leu Met Lys Glu Leu Met
 305 310 315 320
 Glu Leu Ser Glu Pro Glu Arg Ser Ser Arg Trp Leu Arg Cys Cys Phe
 325 330 335
 Val Glu Asp Leu Glu Cys Glu Ile Thr Gln Ile Ala Leu Trp Gln Ala
 340 345 350
 Tyr Gln Ser Arg Phe Ala Asp Pro Arg Leu Pro Gly Gly Gly Val Leu
 355 360 365
 Pro Ala Ala Glu Phe Ile Lys Asn Val Ser Thr Thr Phe Thr Asn Ala
 370 375 380
 Gln Ala Gln Val Ile Asn Gly Pro Gly Ala Ala Thr Lys Phe Ile Ile
 385 390 395 400
 Lys Gly Ile Arg Pro Leu Glu Thr Ala Tyr Thr Phe Glu Gly Phe Pro
 405 410 415
 Tyr Ile Tyr Cys Lys Trp Ala Asp Asn Ser Lys Pro Ser Lys Thr Cys
 420 425 430
 Gln Arg Ala Phe Lys Ser Pro Ala Glu Leu Arg His His Val Phe Thr
 435 440 445
 Glu His Met Asn Leu Lys Pro Thr Glu Thr Pro Gly His Tyr Asn Leu
 450 455 460
 Glu Lys Ala Glu Ser Pro Val His Thr Cys Leu Trp Asp Asn Cys Thr
 465 470 475 480
 Lys Phe Arg Ser Ser Gly Pro Ser Ala Asn Thr Ala Met Val Ala Gly
 485 490 495
 His Val Ser Ala His Leu Pro Glu Glu Arg Ala Pro Asp Ala Glu Pro
 500 505 510
 Pro Thr Ser Lys Arg Ala Val Leu Gln Glu Arg Ile Val Arg Lys Trp
 515 520 525
 Tyr Tyr Leu Asp Thr Pro Val Asn Glu Arg Gly Glu Pro Phe Gly Val
 530 535 540
 Ala Tyr Lys Ala Ala Leu Val Leu Arg Asn Leu Ala Arg Asn Leu Pro

545 550 555 560
 Thr Gly Ile Ala Pro Gln Tyr Asn Gly Leu Ser Trp Lys Lys Ala Val
 565 570 575
 Phe Leu Ser His Arg Pro Lys Ile Ile Glu Ala Trp Asp Arg Asn Arg
 580 585 590
 Ser Leu Arg Lys Glu Leu Thr Glu Leu Ile Met Val Ile Glu Lys Glu
 595 600 605
 Asp Tyr Tyr
 610

<210> 25

<211> 1542

<212> DNA

<213> *Aspergillus fumigatus*

<400> 25

```

atggtctaca tcggcatccc caagaactac acggcttcgc cgtcttcctt tgccggaact 60
ccgtccttga cgatcaatta cgaggcaacg caggatcttg attctaccaa tgcttttgaa 120
ggtttggtga cgccggtgac acgtgtgaga gcagcgtg acagaggctg acagtctaca 180
gggtccagaga aactcttgga ggtgtggttc gcgccttcgc ctcaggaatt aggtccagcg 240
cagcccgcgc gtctgaaggc tggtccggag gagatctgga aggacatgtt ggatctcgtc 300
aattgccagg tcctctcgat tgtttcgtca gaggatgtgg acgcctacct gctctccgag 360
tctagcatgt tcggttggtc tcacaaactc atcttgaaga cttgtggtac caccactctt 420
ctgtctggtc tccacgcgat tctcgagatt gccgctttgt tcggtggctt cccaagtct 480
accgcccctt ctgcgcgaat ctccgtcgcc gctgcgcctt accgcgtctt ctacagccgc 540
aagaacttcc tggtccccga ccgccagcgg ggccctcacc gcagctggag agatgaagtg 600
cggactatgg ataagctctt cctcaacggc agcgcctaca tgattggcaa gatgaatggc 660
gagcactggg acttgtagct gactgaacct cataccatgc tcaccccgcc aacgagcccg 720
ggagccaaga ccgagtttac ggaaacggag accaaggtcc tcagtgtacc ccagggcgct 780
gctctgcaga ctgattcgga ggatgagact ttggaagtct tgatgaccga cttggatgag 840
gagaacgcca agcagttcta cctcgagaat gccactgccc ttgcggagaa ccgttatcgc 900
aactcaaatt cggagaagag tggccatggt gatgttttca gcaacacttc ctccgatata 960
agcgattttg actccgacgg aagccaggtt ctgcctccag agttgactac cgagggtcac 1020
gcgctcgga ccgtggtctc tgaagcctgt ggactttcct ctgtgtatcc taaggagaag 1080
tatcccgatt cgcgcacgca tgcctacctg tttacaccat gcggttctc cgccaacggc 1140
gtgattccgc ctctgaggg aaaagctgga acccactact tcacagtaca cgtcactcca 1200
gagccgcact gttcatatgc gtcctttgag accaactgac cgcactcgca gaacggccag 1260
actaccgctg gaatcatcaa gcaagtggtc gacatcttca agcctggtcg cttcagcgctg 1320
actctcttcg aggccaagcc agcgtgagc caggtcgaag acgagtggaa ggaagccaag 1380
tacctggccg ctgcgcggac cgccaaaatg gaacatgtgg agggatatcg ccgagtggac 1440
cggattgtcc acgacctcga cggctatgag cttgtcttcc gctattatga acgcctggac 1500
tgaaaagggg gggcccctcg gctgggagag gagagatctt ga 1542

```

<210> 26

<211> 1479

<212> DNA

<213> *Aspergillus fumigatus*

<400> 26

```

atggtctaca tcggcatccc caagaactac acggcttcgc cgtcttcctt tgccggaact 60
ccgtccttga cgatcaatta cgaggcaacg caggatcttg attctaccaa tgcttttgaa 120
gggtccagaga aactcttgga ggtgtggttc gcgccttcgc ctcaggaatt aggtccagcg 180
cagcccgcgc gtctgaaggc tggtccggag gagatctgga aggacatgtt ggatctcgtc 240
aattgccagg tcctctcgat tgtttcgtca gaggatgtgg acgcctacct gctctccgag 300

```



```

tctagcatgt tcgtttggcc tcacaaactc atcttgaaga cttgtggtac caccactctt 360
ctgtctgggc tcccaagcat tctcgagatt gccgctttgt tcggtggctt cccaagtct 420
accgcccctt ctgcggaat ctccgctgcc gctgcgccct accgctctt ctacagccgc 480
aagaacttcc tgttccccga ccgccagcgg ggccctcacc gcagctggag agatgaagtg 540
cggactatgg ataagctctt cctcaacggc agcgcctaca tgattggcaa gatgaatggc 600
gagcactggg acttgtacct gactgaacct cataccatgc tcaccccgcc aacgagcccg 660
ggagccaaga ccgagtttac ggaaacggag accaaggctc tcagtgtacc ccagggcgct 720
gctctgcaga ctgattcgga ggatgagact ttggaagtct tgatgaccga cttggatgag 780
gagaacgcca agcagttcta cctcgagaat gccactgccg ttgcggagaa ccgttatcgc 840
aactcaaatt cggagaagag tggccatgtt gatgttttca gcaacacttc ctccgatatc 900
agcgattttg actccgacgg aagccaggtt ctgcctccag agttgactac cgaggggtcac 960
gcgctcgaa ccgtgggtct tgaagcctgt ggactttcct ctgtgtatcc taaggagaag 1020
tatcccgatt cgcgcacga tgacctctg tttacaccat gcggcttctc cgccaacggc 1080
gtgattccgc ctctgaggg aaaagctgga acccactact tcacagtaca cgtcactcca 1140
gagccgcaat gttcatatgc gtcctttgag accaacgtac cgactcgca gaacggccag 1200
actaccgctg gaatcatcaa gcaagtggc gacatcttca agcctggctg cttcagcgtg 1260
actctcttcg aggccaagcc agcgtgagc caggtcgaag acgagtggaa ggaagccaag 1320
tacctggccg ctgcgcggac cgccaaaatg gaacatgtgg agggatatcg ccgagtggac 1380
cggattgtcc acgacctcga cggctatgag cttgtcttcc gctattatga acgcctggac 1440
tggaaagggg gggcccctcg gctgggagag gagagatct 1479

```

<210> 27

<211> 493

<212> PRT

<213> *Aspergillus fumigatus*

<400> 27

```

Met Val Tyr Ile Gly Ile Pro Lys Asn Tyr Thr Ala Ser Pro Ser Ser
 1                5                10                15

Phe Ala Gly Thr Pro Ser Leu Thr Ile Asn Tyr Glu Ala Thr Gln Asp
      20                25                30

Leu Asp Ser Thr Asn Ala Phe Glu Gly Pro Glu Lys Leu Leu Glu Val
      35                40                45

Trp Phe Ala Pro Ser Ala Gln Glu Leu Gly Pro Ala Gln Pro Ala Gly
      50                55                60

Leu Lys Ala Val Pro Glu Glu Ile Trp Lys Asp Met Leu Asp Leu Val
      65                70                75                80

Asn Cys Gln Val Leu Ser Ile Val Ser Ser Glu Asp Val Asp Ala Tyr
      85                90                95

Leu Leu Ser Glu Ser Ser Met Phe Val Trp Pro His Lys Leu Ile Leu
      100                105                110

Lys Thr Cys Gly Thr Thr Thr Leu Leu Ser Gly Leu Pro Arg Ile Leu
      115                120                125

Glu Ile Ala Ala Leu Phe Gly Gly Phe Pro Lys Ser Thr Ala Pro Ser
      130                135                140

Arg Gly Ile Ser Val Ala Ala Ala Pro Tyr Arg Val Phe Tyr Ser Arg
      145                150                155                160

Lys Asn Phe Leu Phe Pro Asp Arg Gln Arg Gly Pro His Arg Ser Trp
      165                170                175

```

Arg Asp Glu Val Arg Thr Met Asp Lys Leu Phe Leu Asn Gly Ser Ala
 180 185 190
 Tyr Met Ile Gly Lys Met Asn Gly Glu His Trp Tyr Leu Tyr Leu Thr
 195 200 205
 Glu Pro His Thr Met Leu Thr Pro Pro Thr Ser Pro Gly Ala Lys Thr
 210 215 220
 Glu Phe Thr Glu Thr Glu Thr Lys Val Leu Ser Val Pro Gln Gly Ala
 225 230 235 240
 Ala Leu Gln Thr Asp Ser Glu Asp Glu Thr Leu Glu Val Leu Met Thr
 245 250 255
 Asp Leu Asp Glu Glu Asn Ala Lys Gln Phe Tyr Leu Glu Asn Ala Thr
 260 265 270
 Ala Val Ala Glu Asn Arg Tyr Arg Asn Ser Asn Ser Glu Lys Ser Gly
 275 280 285
 His Val Asp Val Phe Ser Asn Thr Ser Ser Asp Ile Ser Asp Phe Asp
 290 295 300
 Ser Asp Gly Ser Gln Val Leu Pro Pro Glu Leu Thr Thr Glu Gly His
 305 310 315 320
 Ala Leu Gly Thr Val Val Ser Glu Ala Cys Gly Leu Ser Ser Val Tyr
 325 330 335
 Pro Lys Glu Lys Tyr Pro Asp Ser Arg Ile Asp Ala Tyr Leu Phe Thr
 340 345 350
 Pro Cys Gly Phe Ser Ala Asn Gly Val Ile Pro Pro Pro Glu Gly Lys
 355 360 365
 Ala Gly Thr His Tyr Phe Thr Val His Val Thr Pro Glu Pro His Cys
 370 375 380
 Ser Tyr Ala Ser Phe Glu Thr Asn Val Pro His Ser Gln Asn Gly Gln
 385 390 395 400
 Thr Thr Ala Gly Ile Ile Lys Gln Val Val Asp Ile Phe Lys Pro Gly
 405 410 415
 Arg Phe Ser Val Thr Leu Phe Glu Ala Lys Pro Ala Leu Ser Gln Val
 420 425 430
 Glu Asp Glu Trp Lys Glu Ala Lys Tyr Leu Ala Ala Arg Arg Thr Ala
 435 440 445
 Lys Met Glu His Val Glu Gly Tyr Arg Arg Val Asp Arg Ile Val His
 450 455 460
 Asp Leu Asp Gly Tyr Glu Leu Val Phe Arg Tyr Tyr Glu Arg Leu Asp
 465 470 475 480
 Trp Lys Gly Gly Ala Pro Arg Leu Gly Glu Glu Arg Ser
 485 490

<210> 28
 <211> 637
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 28
 atgggtcgcg ttagaaccac ggtaagttac agatgaagca tcatgagtta tcttcaaaaa 60
 agccccaata gagtatcatt tctgacgaaa tgggtttttc ttcaatagac agtcaagagg 120
 tccgccaagg tcatcatcga gcgctactac cccaagttga cgctcgactt tgagaccaac 180
 aagcgtcttt gcgatgagat cgctatcatt gcctccaagc gccttcgcaa caaggtgggc 240
 aatccatcac tgagccgtac aacagtcgga atttgacttg ctgacgaaaa ctgatttgct 300
 ggttacacca cccaccttat gaagcgtatc cagcgtggcc ctgtccgcgg tatctcttct 360
 aagctgcagg aggaggagcg tgagcgcaag gatcagtagc ttccctgagg ttccgctctg 420
 gatgtttccc agaccgagtc cggccagctc gatgtcgatg ccgacacca ggaccttctc 480
 aagtccatgg gcgtaagttc tgttctcaac gcggttggtc gtggttttaa agcagtcctg 540
 taacttatat tgcccactac agttcgacaa tctcaaggtc aacgttgtca acgtctccca 600
 acatcagggt caggagcgcc cccgcccgtt ccggtag 637

<210> 29
 <211> 417
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 29
 atgggtcgcg ttagaaccac gacagtcaag aggtccgccca aggtcatcat cgagcgctac 60
 taccccaagt tgacgctcga ctttgagacc aacaagcgtc tttgcatga gatcgctatc 120
 attgcctcca agcgccttcg caacaagatt gctggttaca ccaccacct tatgaagcgt 180
 atccagcgtg gccctgtccg cggtatctct tccaagctgc aggaggagga gcgtgagcgc 240
 aaggatcagt acgttcctga ggtttccgct ctggatgttt cccagaccga gtccggccag 300
 ctgatgtcgc atgccgacac caaggacctt ctcaagtcca tgggcttcga caatctcaag 360
 gtcaacggtg tcaacgtctc ccaacatcag gttcaggagc gcccccgccg cttccgg 417

<210> 30
 <211> 139
 <212> PRT
 <213> *Aspergillus fumigatus*

<400> 30
 Met Gly Arg Val Arg Thr Lys Thr Val Lys Arg Ser Ala Lys Val Ile
 1 5 10 15
 Ile Glu Arg Tyr Tyr Pro Lys Leu Thr Leu Asp Phe Glu Thr Asn Lys
 20 25 30
 Arg Leu Cys Asp Glu Ile Ala Ile Ala Ser Lys Arg Leu Arg Asn
 35 40 45
 Lys Ile Ala Gly Tyr Thr Thr His Leu Met Lys Arg Ile Gln Arg Gly
 50 55 60
 Pro Val Arg Gly Ile Ser Phe Lys Leu Gln Glu Glu Glu Arg Glu Arg
 65 70 75 80
 Lys Asp Gln Tyr Val Pro Glu Val Ser Ala Leu Asp Val Ser Gln Thr
 85 90 95
 Glu Ser Gly Gln Leu Asp Val Asp Ala Asp Thr Lys Asp Leu Leu Lys
 100 105 110

Ser Met Gly Phe Asp Asn Leu Lys Val Asn Val Val Asn Val Ser Gln
 115 120 125

His Gln Val Gln Glu Arg Pro Arg Arg Phe Arg
 130 135

<210> 31

<211> 1035

<212> DNA

<213> *Aspergillus fumigatus*

<400> 31

```
atggcggttg gaaagtatgc caattcactt ctattattgt tctgaacgct tttagcatgt 60
gtctggatac ggtgggtttac aggtactgat ccgggaacag gaacaagcgc ttgtcgaagg 120
gcaagaaggg tgtaagaag aggaccgttg atcctttctc caggaaggac gaatactctg 180
ttaaggtagt tcgacgtgga ctgtgtaagt cgaccgcagc taatctatat caggcgcctt 240
ccactttcca gatcagagag tatgttgac gcatatgat tcgaatgcag gataaaggcg 300
attcacaatg gtagtggaga ttatgctgac tgaattatag tgtcgggaag actctgggtca 360
accgcaccag tgggtctcaag aacgccaatg actccctgaa gggtcgaatt ttcgaggtct 420
cgctggctga cctgcagaat gatgaagacc atgctttccg caaggttaag cttcgtgtgg 480
acgaggttca gggcaagaac tgtttgacca acttccacgg tcttgatttc acaaccgaca 540
aattgcgac cctcgtgcgc aagtggcagt cgctgatcga agccatgtca ctgtgaagac 600
gaccgatgat tatctccttc ggctttttgc tatcgcttc accaagagac gcccgacca 660
gattaagaag accacatatg ctctgtcttc tcaaatccgt gccatccgca agaagatgat 720
tctgaggtc attggtcgtg agatcgagaa ggctaccag ggaatctatc ctttgcagaa 840
tgtgtgtgac cctgttattc ttactcggga tgaagactaa ctgcaatcta ggtccatatt 900
cgcaaggtca agcttcttaa ggctcccaag ttcgacctgg gtgcaactgt gaatctgcac 960
ggtgaatcta caaccgatga taagggccac aaggctcgaga gagagttoaa ggagcaggtt 1020
ctcgaaagcg ttttaa 1035
```

<210> 32

<211> 768

<212> DNA

<213> *Aspergillus fumigatus*

<400> 32

```
atggcggttg gaaagaacaa gcgcttgtcg aagggaaga aggggtgtta gaagaggacc 60
gttgatcctt tctccaggaa ggacgaatac tctgttaagg cgccttcac tttccagatc 120
agagatgtcg ggaagactct ggtcaaccgc accagtgggt tcaagaacgc caatgactcc 180
ctgaagggtc gaattttcga ggtctcgctg gctgacctgc agaagatga agaccatgct 240
ttccgcaagg ttaagcttcg tgtggacgag gttcagggca agaactgttt gaccaacttc 300
cacggtcttg atttcacaac cgacaaattg cgatccctcg tgcgcaagtg gcagtcgctg 360
atcgaagcca atgtcactgt gaagacgacc gatgattatc tccttcggct ttttgctatc 420
gccttcacca agagacgccc gaaccagatt aagaagacca catatgctcg ttcttctcaa 480
atccgtgcc a tccgcaagaa gatgattgaa atcatgcaga gggaggcagc cagctgctct 540
ctcgctcagc tcactcacia gctcattcct gaggtcattg gtcgtgagat cgagaaggct 600
accagggaa tctatccttt gcagaatgtc catattcgca aggtcaagct tcttaaggct 660
cccaagttcg acctgggtgc actgctgaat ctgcacggtg aatctacaac cgatgataag 720
ggccacaagg tcgagagaga gttcaaggag caggttctcg aaagcgtt 768
```

<210> 33

<211> 256

<212> PRT

<213> *Aspergillus fumigatus*

<400> 33

Met Ala Val Gly Lys Asn Lys Arg Leu Ser Lys Gly Lys Lys Gly Val
 1 5 10 15

Lys Lys Arg Thr Val Asp Pro Phe Ser Arg Lys Asp Glu Tyr Ser Val
 20 25 30

Lys Ala Pro Ser Thr Phe Gln Ile Arg Asp Val Gly Lys Thr Leu Val
 35 40 45

Asn Arg Thr Ser Gly Leu Lys Asn Ala Asn Asp Ser Leu Lys Gly Arg
 50 55 60

Ile Phe Glu Val Ser Leu Ala Asp Leu Gln Asn Asp Glu Asp His Ala
 65 70 75 80

Phe Arg Lys Val Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Cys
 85 90 95

Leu Thr Asn Phe His Gly Leu Asp Phe Thr Thr Asp Lys Leu Arg Ser
 100 105 110

Leu Val Arg Lys Trp Gln Ser Leu Ile Glu Ala Asn Val Thr Val Lys
 115 120 125

Thr Thr Asp Asp Tyr Leu Leu Arg Leu Phe Ala Ile Ala Phe Thr Lys
 130 135 140

Arg Arg Pro Asn Gln Ile Lys Lys Thr Thr Tyr Ala Arg Ser Ser Gln
 145 150 155 160

Ile Arg Ala Ile Arg Lys Lys Met Ile Glu Ile Met Gln Arg Glu Ala
 165 170 175

Ala Ser Cys Ser Leu Ala Gln Leu Thr His Lys Leu Ile Pro Glu Val
 180 185 190

Ile Gly Arg Glu Ile Glu Lys Ala Thr Gln Gly Ile Tyr Pro Leu Gln
 195 200 205

Asn Val His Ile Arg Lys Val Lys Leu Leu Lys Ala Pro Lys Phe Asp
 210 215 220

Leu Gly Ala Leu Leu Asn Leu His Gly Glu Ser Thr Thr Asp Asp Lys
 225 230 235 240

Gly His Lys Val Glu Arg Glu Phe Lys Glu Gln Val Leu Glu Ser Val
 245 250 255

<210> 34

<211> 614

<212> DNA

<213> *Aspergillus fumigatus*

<400> 34

cctgtcggag atgatcaaag gcagcacctc gaattttcga ggaacactgc gaatagtttc 60

```

aatcatgtat atggacccat tttcccgta ccagaagcaa ttatatgtaa gtgggtttttg 120
cttctggcgg aacggtcctg tgttgggaaa ttgacggcta tcaatagcgc ctgctaaacg 180
ggttatgtcc ctcaaagaac cgacgttgaa aatgtccaag tcccatgccg acagacgctc 240
aaggatcatt cttacggatt cgcccgagaa aatctccaaa aagatcaatg ctgcgctcac 300
agactcggaa ttaaccatta catatgaccc agtccgtcga cctggagtgg cgaatttaat 360
agagatcttg agtcacttcg atggacgaac ttgcatgag attgccatgg aataccgttc 420
agccagtctt cgcgctctaa aggaacatct ggccagaacg ttgtccaatc atcttgagcc 480
aataagagag aagtatctct cactttagg agatcagact gactaccttg attctatagc 540
agaacagggt tctgaagccg cgcgggcaac cgctgaattg acaatggagc aagtcaaagt 600
cgctatgggc ttaa                                     614

```

<210> 35

<211> 552

<212> DNA

<213> *Aspergillus fumigatus*

<400> 35

```

cctgtcggag atgatcaaag gcagcacctc gaattttcga ggaacactgc gaatagtttc 60
aatcatgtat atggacccat tttcccgta ccagaagcaa ttatatcgcc tgctaaacgg 120
gttatgtccc tcaaagaacc gacgttgaaa atgtccaagt cccatgccga cagacgctca 180
aggatcattc ttacggattc gcccgcagaa atctccaaaa agatcaatgc tgcgctcaca 240
gactcggaa taaccattac atatgaccca gtccgtcgac ctggagtggc gaatttaata 300
gagatcttga gtcacttcga tggacgaact tgcgatgaga ttgccatgga ataccgttca 360
gccagtcttc gcgctctaaa ggaacatctg gccagaacgt tgtccaatca tcttgagcca 420
ataagagaga agtatctctc actttaggga gatcagactg actaccttga ttctatagca 480
gaacagggtt ctgaagccgc gcgggccaac gctgaattga caatggagca agtcaaagtc 540
gctatgggct ta                                     552

```

<210> 36

<211> 184

<212> PRT

<213> *Aspergillus fumigatus*

<400> 36

```

Pro Val Gly Asp Asp Gln Arg Gln His Leu Glu Phe Ser Arg Asn Thr
 1             5             10             15

Ala Asn Ser Phe Asn His Val Tyr Gly Pro Ile Phe Pro Ser Pro Glu
      20             25             30

Ala Ile Ile Ser Pro Ala Lys Arg Val Met Ser Leu Lys Glu Pro Thr
      35             40             45

Leu Lys Met Ser Lys Ser His Ala Asp Arg Arg Ser Arg Ile Ile Leu
 50             55             60

Thr Asp Ser Pro Ala Glu Ile Ser Lys Lys Ile Asn Ala Ala Leu Thr
 65             70             75             80

Asp Ser Glu Leu Thr Ile Thr Tyr Asp Pro Val Arg Arg Pro Gly Val
      85             90             95

Ala Asn Leu Ile Glu Ile Leu Ser His Phe Asp Gly Arg Thr Cys Asp
      100            105            110

Glu Ile Ala Met Glu Tyr Arg Ser Ala Ser Leu Arg Ala Leu Lys Glu
      115            120            125

His Leu Ala Arg Thr Leu Ser Asn His Leu Glu Pro Ile Arg Glu Lys

```

130

135

140

Tyr Leu Ser Leu Val Gly Asp Gln Thr Asp Tyr Leu Asp Ser Ile Ala
 145 150 155 160

Glu Gln Gly Ser Glu Ala Ala Arg Ala Asn Ala Glu Leu Thr Met Glu
 165 170 175

Gln Val Lys Val Ala Met Gly Leu
 180

<210> 37

<211> 819

<212> DNA

<213> *Aspergillus fumigatus*

<400> 37

```

atggcaactt cgactgggac cggatgggct cagctccggc agcaagcccg ttcgcttgag 60
actcaggtac ggaactcgaa actacgctat aatgaggctt tactcgtgat ttggatgttg 120
acaataatgt tcctagaccg agagtctgtt tcacacctat gcgcagtatg catcgatgac 180
gaagctgcct ccgaaaccct cagaagaaga acaacggatt gaatcgcaac tgaaggatct 240
tcttgaaaag gtgtgcactt tgaggccctc tagtccagcc caacagacga tcatgctgac 300
acgatccgat catagcgtga agccctcatc tcccagctct cccgtctcct tgactccgaa 360
gccactctta ccgcatctgc cctgaaacag agcaatcttg cccgcaatcg cgaagtcctc 420
caggatcatc gccgcgaatt gcagcgccctg aacgccgcaa tcgccgagtc ccgcgaccga 480
gccaatcttc tgtctaacgt ccgctccgac attgatgcct accgcaattc aaaccccgcc 540
gcggctgagg cagactacat gctcgaggag cggggctcgta tagatgaaag ccataacatg 600
atagatgggt tcctaagcca ggcgtatgca atcaacgaga gttttgggct acaacgtgaa 660
accctggcca gcatcaatcg ccgtatcgtc ggtgctgcca ataaggtacc aggaatgaat 720
gcattgattg gtaagattgg gacgaagagg agacgtgacg caatcatctt gggggctttc 780
atcggcctttt gtttcttgat ggtgttcttc ttccgatga 819

```

<210> 38

<211> 681

<212> DNA

<213> *Aspergillus fumigatus*

<400> 38

```

atggcaactt cgactgggac cggatgggct cagctccggc agcaagcccg ttcgcttgag 60
actcagaccg agagtctgtt tcacacctat gcgcagtatg catcgatgac gaagctgcct 120
ccgaaaccct cagaagaaga acaacggatt gaatcgcaac tgaaggatct tcttgaaaag 180
cgtgaagccc tcatctccca gctctccgct ctcccttgact ccgaagccac tcttaccgca 240
tctgccctga aacagagcaa tcttgccgcg aatcgcgaaag tcctccagga tcatcgccgc 300
gaattgcagc gcctgaacgc cgcaatcgcc gagtcccgcg accgagccaa tcttctgtct 360
aacgtccgct ccgacattga tgcctaccgc aattcaaacc ccgccgcggc tgaggcagac 420
tacatgctcg aggagcgggg tcgtatagat gaaagccata acatgataga tgggtgccta 480
agccaggcgt atgcaatcaa cgagagtttt gggctacaac gtgaaaccct ggccagcatc 540
aatcgccgta tcgtcggtgc tgccaataag gtaccaggaa tgaatgcatt gattggtaag 600
attgggacga agaggagacg tgacgcaatc atcttggggg ctttcatcgg cttttgtttc 660
ttgatggtgt tcttcttccg a 681

```

<210> 39

<211> 227

<212> PRT

<213> *Aspergillus fumigatus*

<400> 39

Met Ala Thr Ser Thr Gly Thr Gly Trp Ala Gln Leu Arg Gln Gln Ala
 1 5 10 15
 Arg Ser Leu Glu Thr Gln Thr Glu Ser Leu Phe His Thr Tyr Ala Gln
 20 25 30
 Tyr Ala Ser Met Thr Lys Leu Pro Pro Lys Pro Ser Glu Glu Glu Gln
 35 40 45
 Arg Ile Glu Ser Gln Leu Lys Asp Leu Leu Glu Lys Arg Glu Ala Leu
 50 55 60
 Ile Ser Gln Leu Ser Arg Leu Leu Asp Ser Glu Ala Thr Leu Thr Ala
 65 70 75 80
 Ser Ala Leu Lys Gln Ser Asn Leu Ala Arg Asn Arg Glu Val Leu Gln
 85 90 95
 Asp His Arg Arg Glu Leu Gln Arg Leu Asn Ala Ala Ile Ala Glu Ser
 100 105 110
 Arg Asp Arg Ala Asn Leu Leu Ser Asn Val Arg Ser Asp Ile Asp Ala
 115 120 125
 Tyr Arg Asn Ser Asn Pro Ala Ala Ala Glu Ala Asp Tyr Met Leu Glu
 130 135 140
 Glu Arg Gly Arg Ile Asp Glu Ser His Asn Met Ile Asp Gly Val Leu
 145 150 155 160
 Ser Gln Ala Tyr Ala Ile Asn Glu Ser Phe Gly Leu Gln Arg Glu Thr
 165 170 175
 Leu Ala Ser Ile Asn Arg Arg Ile Val Gly Ala Ala Asn Lys Val Pro
 180 185 190
 Gly Met Asn Ala Leu Ile Gly Lys Ile Gly Thr Lys Arg Arg Arg Asp
 195 200 205
 Ala Ile Ile Leu Gly Ala Phe Ile Gly Phe Cys Phe Leu Met Val Phe
 210 215 220
 Phe Phe Arg
 225

<210> 40

<211> 1601

<212> DNA

<213> *Aspergillus fumigatus*

<400> 40

atgtcacaaa atcgacctgg ggtgttctcg aatctgcgca tgggtggtaa ggaacatcca 60
 aatgctgagt ccaattgttc agaaaacatt acccaggagc ctgtggaact aactgctttg 120
 ctttccgacc atacagaagt cgctcgcgag aaggccagg atggactgac aggggaaact 180
 aaggagattt cgtactcaca atgtaaaatc gtcggcaatg gatcgtttgg tgtcgtcttt 240
 cagacgaaaa tgatgccaag cggcgaggat gctgccatta agagggtcct tcaagacaag 300
 cgcttcaaa tatgtgtaca ttataagggc aattgccctc gctgccaac ccaaagatac 360
 tgtcgctgac gagataccag aatcgagaac tgcagattat gcggattgtt cgccatccta 420
 acatcgtaga attgaaagcc ttctattact cgaacggcga gagggtatgc gactctcctt 480


```

tgtctcccca ttcgtttctag tttgccgttt gctgactacc ctaccattgt ctttcacaga 540
aggatgaagt gtacctaaac ctcgttctcg aatacgtaac agaaaccgtg tatcgggcgt 600
cgcggtactt taataaactc aaaacgacta tgccaatgtt ggaagtcaag ctgtatatct 660
atcaattgtt ccgttccctg gcatacatcc attcacaagg catctgccac cgtgacatca 720
agccccagaa tctcttactt gatccatcca ccggcatcct caaactctgc gactttgggt 780
cggccaagat tctggttagag aatgagccca acgtttccta tatctgttcc cgctactatc 840
gtgcgcggga attgatcttt ggcgccacta attacacaac aaagatcggt aagtcttgac 900
tgattcctcc ttcaagtttg gtactgtcat gctgacgac gtcaagacgt gtggtccacg 960
ggttggtgta tggctgaact catgcttggg cagccattgt tccctggaga gtcgggaatt 1020
gaccaactgg tggaaatcat caaggttctt ggaacccta ctcgggagca gatccgcacc 1080
atgaacccaa actatatgga gcacaaattc cctcaaatca agccacaccc attcaacaag 1140
gtgaccacgc tcttaaagaa cttcttgcca atatgcactg acttgatgac ccaggtttt 1200
ccggagagct cctcacgagg ccattgatct gatctcagct ttgctagaat acacgccgac 1260
acaacgtctc tccgctatcg aggcgatgtg ccaccggtt ttcgacgaac tcagagatcc 1320
caatacgcga ctgcccgaact ctcgccaccc tgggtggcgt gctagagacc tccccaatct 1380
ctttgatctt tccagacatg gtttggtgtc acttgaggcc caaattcatt cttccagatg 1440
gcttattcgc tgatcaactct tttgtagaac tttctattgc acctgcattg aacagccggc 1500
tggttcccc tcatgcacgc gccgctctcg aggccgggg gctagacatt gacaacttca 1560
ctcctctcac gaaggaggag atgatggcac gtctcgactg a 1601

```

<210> 41

<211> 1182

<212> DNA

<213> *Aspergillus fumigatus*

<400> 41

```

atgtcacaaa atcgacctgg ggtgttctcg aatctgcgca tgggtgaagt cgtccgcgag 60
aagggtccagg atggactgac aggggaaact aaggagattt cgtactcaca atgtaaaatc 120
gtcggcaatg gatcgttttg tgctgtcttt cagacgaaaa tgatgccaaag cggcgaggat 180
gctgccatta agagggtcct tcaagacaag cgcttcaaaa atcgagaact gcagattatg 240
cggattgttc gccatcctaa catcgtagaa ttgaaagcct tctattactc gaacggcgag 300
aggaaggatg aagtgtacct aaacctcggt ctcgaatacg taccagaaac cgtgtatcgg 360
gcgctgcggg actttaataa actcaaaacg actatgccaa tggttgaagt caagctgtat 420
atctatcaat tggtccgttc cctggcatac atccattcac aaggcatctg ccaccgtgac 480
atcaagcccc agaattctctt acttgatcca tccaccggca tcctcaaact ctgcgacttt 540
ggttcggcca agattctggg agagaatgag cccaacgttt cctatatctg ttcccgtac 600
tatcgtgcgc cggaattgat ctttggcgcc actaattaca caacaaagat cgacgtgtgg 660
tccacggggt gtgtgatggc tgaactcatg cttggtcagc cattgttccc tggagagtcg 720
ggaattgacc aactggtgga aatcatcaag gttcttgaa cccctactcg ggagcagatc 780
cgcaccatga acccaaacta tatggagcac aaattccctc aaatcaagcc acaccattc 840
aacaagggtt tccggagagc tcctcacgag gccattgatc tgatctcagc tttgctagaa 900
tacacgccga cacaacgtct ctccgctatc gaggcgatgt gccaccggtt cttcgacgaa 960
ctcagagatc ccaatacgcg actgcccgcg tctcggcacc ctggtggcgc tgctagagac 1020
ctccccaatc tctttgattt ctccagacat gaactttcta ttgcacctgc attgaacagc 1080
cggctgggtt cccctcatgc acgcgcgct ctcaggccc gggggctaga cattgacaac 1140
ttcactctc tcacgaagga ggagatgatg gcacgtctcg ac 1182

```

<210> 42

<211> 394

<212> PRT

<213> *Aspergillus fumigatus*

<400> 42

```

Met Ser Gln Asn Arg Pro Gly Val Phe Ser Asn Leu Arg Met Gly Glu
  1                      5                      10                      15

```

```

Val Val Arg Glu Lys Val Gln Asp Gly Leu Thr Gly Glu Thr Lys Glu
      20                      25                      30

```

Ile Ser Tyr Ser Gln Cys Lys Ile Val Gly Asn Gly Ser Phe Gly Val
 35 40 45
 Val Phe Gln Thr Lys Met Met Pro Ser Gly Glu Asp Ala Ala Ile Lys
 50 55 60
 Arg Val Leu Gln Asp Lys Arg Phe Lys Asn Arg Glu Leu Gln Ile Met
 65 70 75 80
 Arg Ile Val Arg His Pro Asn Ile Val Glu Leu Lys Ala Phe Tyr Tyr
 85 90 95
 Ser Asn Gly Glu Arg Lys Asp Glu Val Tyr Leu Asn Leu Val Leu Glu
 100 105 110
 Tyr Val Pro Glu Thr Val Tyr Arg Ala Ser Arg Tyr Phe Asn Lys Leu
 115 120 125
 Lys Thr Thr Met Pro Met Leu Glu Val Lys Leu Tyr Ile Tyr Gln Leu
 130 135 140
 Phe Arg Ser Leu Ala Tyr Ile His Ser Gln Gly Ile Cys His Arg Asp
 145 150 155 160
 Ile Lys Pro Gln Asn Leu Leu Leu Asp Pro Ser Thr Gly Ile Leu Lys
 165 170 175
 Leu Cys Asp Phe Gly Ser Ala Lys Ile Leu Val Glu Asn Glu Pro Asn
 180 185 190
 Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala Pro Glu Leu Ile Phe
 195 200 205
 Gly Ala Thr Asn Tyr Thr Thr Lys Ile Asp Val Trp Ser Thr Gly Cys
 210 215 220
 Val Met Ala Glu Leu Met Leu Gly Gln Pro Leu Phe Pro Gly Glu Ser
 225 230 235 240
 Gly Ile Asp Gln Leu Val Glu Ile Ile Lys Val Leu Gly Thr Pro Thr
 245 250 255
 Arg Glu Gln Ile Arg Thr Met Asn Pro Asn Tyr Met Glu His Lys Phe
 260 265 270
 Pro Gln Ile Lys Pro His Pro Phe Asn Lys Val Phe Arg Arg Ala Pro
 275 280 285
 His Glu Ala Ile Asp Leu Ile Ser Ala Leu Leu Glu Tyr Thr Pro Thr
 290 295 300
 Gln Arg Leu Ser Ala Ile Glu Ala Met Cys His Pro Phe Phe Asp Glu
 305 310 315 320
 Leu Arg Asp Pro Asn Thr Arg Leu Pro Asp Ser Arg His Pro Gly Gly
 325 330 335
 Ala Ala Arg Asp Leu Pro Asn Leu Phe Asp Phe Ser Arg His Glu Leu
 340 345 350
 Ser Ile Ala Pro Ala Leu Asn Ser Arg Leu Val Pro Pro His Ala Arg

355

360

365

Ala Ala Leu Glu Ala Arg Gly Leu Asp Ile Asp Asn Phe Thr Pro Leu
 370 375 380

Thr Lys Glu Glu Met Met Ala Arg Leu Asp
 385 390

<210> 43

<211> 2209

<212> DNA

<213> *Aspergillus fumigatus*

<400> 43

```

accgcgcgat cctgctgtgc tgagtcagca ttggattact tcattagacc tcgacagtca 60
acagcatttc tccacttaac cacctacaac ctaagacagc acgggaactg gttatatttg 120
ttcgagtcag ttacttcagg gtgttttatt aaatcaatgt ggaagtcttt taaagaaaag 180
catgccagca agtttggggg aggctcggct gaagcggcag cctcagacgg tggccaagat 240
ctgaccagca tattggatag atcccaacgc gggaattga cagtgcctgt tgcgctaata 300
gcacagcgga tgcgggatgg aatagaacaa aacttctcca atgctcctcc ttcgtcaggc 360
cagtctgtca actacgaaga aaaacggaca ggctccctgc cccaatctac agatgcacaa 420
gaagaccagt catcctccgg cagcgcagcg aacggttcaa gaaccgaccc tcaattcaaa 480
gacccggaga ctgcgacatg tgcactatct aaatatgat actggaggga ctccgtcctt 540
cttcgaattg gtgaagtcgt caacagggat ccagaacatg gtgaagttca ggcgaatgaa 600
aaccacacct caggacagca atcccagcag atccgctccg aggaggatga ccgttccatt 660
cgtaagctac gtgaggtctt tccgccgggt gagaccagcc tctctcaatt gccagaagcg 720
aagaaactct taattctcca ctcatgtcta ctctagttt tgagtcctga acactataac 780
gcctggctct gggtcctgat gctgttcgtg acgtccagct tagggctgga cgtgaaatta 840
ctaaacgaag atgaagtcaa agtggcgagg ggggttgctt acactgctct ggactgtcg 900
tctaacgccc caaggcagga tgagagtcga agtcgcgatt catcccgaaa atggaaggtt 960
gggatcgctg cagttgcggg tgcgtgccctg atcgggatca ctggtggact ggctgcgccc 1020
cttggtgcag ctgggcttgg tactgtcatg ggcggccttg ggcttggcgc caccgccgca 1080
gcagggatgc tcggagctct cgctggaagt ggtgttgctg tcggcggact tttcggtgct 1140
tatggtgggc ggatgaccgg tcgtatgggt gacaagtaag cacgggaggt ggatgatttt 1200
gcctttctgc cgattcgtgg ttctcggcat cgatccgaag acgaaagaga agctgcccac 1260
caggatcacc ggctgcgggt taccatcggc gtgaccggat ggctgacaga ggaggacaat 1320
ttcgtgatcc cgtggcgagt gatcggagcg gaatcggagg tgtttggtct ccgctgggaa 1380
accgagcccc tgatgaatct gggaaatgcg cttgaccttt tggttaaccag cgccgcatgg 1440
actgccggtg aacaagtcct gaagaagaca ttctctccc aactcttgac cgctgtcgcg 1500
ctgccgcttg gccttctcaa ggtcgcacgt gtggtggaca atccgtttag cgtagcgaag 1560
gctcgggagg acaaggctgg ggaggttctc gcggtgctc ttatcagtaa agtgcagggc 1620
gagcgaccag tcaccctcat tggetactcc ttaggtctc gggtgatttt cgcttgccct 1680
caaagcttgg cgaaacggcg cgcgttcggc ttggtggaat ccgcaattct gatgggagct 1740
cccaccccggt cgaattcaga acaatggtgt cgcctccgca gtgttgtag tggacgcctt 1800
gtcaacgtgt actcgaaaaa cgactccgtg ctggctctct tatatcgaa aagcagcctc 1860
cagcttgggg ttgcaggctt gcagcctgtt gaaggtgtct caggcgttga gaatctggac 1920
gttagcgacc tgatcagcgg ccactctcgt tatcagtttc tcgttggcag gatcttgagc 1980
gttggttgac ttgagagcat tgatgctcgc gaggtcgcac tggaggaggc cgcattagaa 2040
gccaaagatc ggaggcagga gcaggaaaagg gctcataacg aacgacaggc tggatttatg 2100
ggcgagggtc ggtcaccaag ccagcggctg gaaagccagg aggatctgca gggcgaagag 2160
gacagattac agaaagagat gggaaaagca cgagtgcggc actcttaga 2209

```

<210> 44

<211> 2209

<212> DNA

<213> *Aspergillus fumigatus*

<400> 44

```

accgcgcgat cctgctgtgc tgagtcagca ttggattact tcattagacc tgcacagtca 60
acagcatttc tccacttaac cacctacaac ctaagacagc acgggaactg gttatatattg 120
ttcagatcag ttacttcagg gtgttttatt aaatcaatgt ggaagtcttt taaagaaaag 180
catgccagca agtttggggg aggtcggcgt gaagcggcag cctcagacgg tggccaagat 240
ctgaccagca tattggatag atcccaacgc ggggaattga cagtgtctgt tgcgctaatac 300
gcacagcggg tgcgggatgg aatagaacaa aacttctcca atgctcctcc ttcgtcaggc 360
cagtctgtca actacgaaga aaaacggaca ggctccctgc cccaatctac agatgcacaa 420
gaagaccagt catcctccgg cagcgcagcg aacggttcaa gaaccgaccc tcaattcaaa 480
gaccgcggaga ctgcgacatg tgcactatct aaatatgatg actggaggga ctccgtcctt 540
cttcgaattg gtgaagtcgt caacagggat ccagaacatg gtgaagttca ggcgaatgaa 600
aaccacacct caggacagca atcccagcag atccgctccg aggaggatga ccgttccatt 660
cgtaagctac gtgaggtctt tccgcccgtg gagaccagcc tctctcaatt gccagaagcg 720
aagaaactct taattctcca ctcatgtcta ctctagttt tgagtcttga aactataaac 780
gcctggtctc gggctctgat gctgttcgtg acgtccagct tagggctgga cgtgaaatta 840
ctaaacgaag atgaagtcaa agtggcagag ggggtgcttg acactgctct ggcaactgtc 900
tctaacgccc caaggcagga tgagagtcga agtcgcgatt catcccgaaa atggaaggtt 960
gggatcgcgt cagttgcggg tgctgccctg atcgggatca ctggtggact ggctgcgccc 1020
cttggtgcag ctgggcttgg tactgtcatg ggcgcccttg ggcttggcgc caccgcccga 1080
gcagggtatc tcggagctct cgctggaagt ggtgtgtgct tcggcggact tttcgggtgct 1140
tatggtgggg ggatgaccgg tcgtatggtt gacaagtacg cacgggaggt ggatgatttt 1200
gcctttctgc cgattcgtgg ttctcggcat cgatccgaag acgaaagaga agctgcccac 1260
caggatcacc ggctgcgggt taccatcggc gtgaccgat ggctgacaga ggaggacaat 1320
ttcgtgatcc cgtggcgagt gatcggagcg gaatcggagg tgtttggtct ccgctgggaa 1380
accgagcccc tgatgaatct gggaaatgcg cttgaccttt tggttaaccag cgccgcatgg 1440
actgccggtg aacaagtcct gaagaagaca ttctctctcc aactcttgac cgctgtcgcg 1500
ctgccgcttg gccttctcaa ggtcgcacgt gtggtggaca atccgtttag cgtagcgaag 1560
gctcggggcg acaaggctgg ggaggttctc gcggatgctc ttatcagtaa agtgcaggcg 1620
gagcgaccag tcaccctcat tggctactcc ttagggtctc ggggtgatttt cgcttgccct 1680
caaagcttgg cgaaacggcg cgcgttcggc ttggtggaat ccgcaattct gatgggagct 1740
cccaccccg tgaattcaga acaatggtgt cgcacccgca gtgttggtgag tggacgcctt 1800
gtcaacgtgt actcgaaaaa cgactccgtg ctggctctct tatatcgaa aagcagcctc 1860
cagcttgggg ttgcaggctt gcagcctgtt gaaggtgtct caggcgttga gaactctggac 1920
gttagcgacc tgatcagcgg ccactcctcg tatcagtttc tcgttggcag gatcttgagc 1980
gttggtggac ttgagagcat tgatgctcgc gaggtcgcac tggaggaggc cgcattagaa 2040
gccaaagatc ggaggcagga gcaggaaagg gctcataacg aacgacaggc tggatttatg 2100
ggcgagggtc ggtcaccaag ccagcggctg gaaagccagg aggatctgca gggcgaagag 2160
gacagattac agaaaagatg gggaaaagca cgagtgcggc actcttaga 2209

```

<210> 45

<211> 735

<212> PRT

<213> *Aspergillus fumigatus*

<400> 45

Thr Ala Arg Ser Cys Cys Ala Glu Ser Ala Leu Asp Tyr Phe Ile Arg
1 5 10 15

Pro Arg Gln Ser Thr Ala Phe Leu His Leu Thr Thr Tyr Asn Leu Arg
20 25 30

Gln His Gly Asn Trp Leu Tyr Leu Phe Glu Ser Val Thr Ser Gly Cys
35 40 45

Phe Ile Lys Ser Met Trp Lys Ser Phe Lys Glu Lys His Ala Ser Lys
50 55 60

Phe Gly Gly Gly Ser Ala Glu Ala Ala Ala Ser Asp Gly Gly Gln Asp
65 70 75 80

Leu Thr Thr Ile Leu Asp Arg Ser Gln Arg Gly Glu Leu Thr Val Leu

41/169

Glu Ala Ala His Gln Asp His Arg Leu Arg Val Thr Ile Gly Val Thr
 420 425 430
 Gly Trp Leu Thr Glu Glu Asp Asn Phe Val Ile Pro Trp Arg Val Ile
 435 440 445
 Gly Ala Glu Ser Glu Val Phe Gly Leu Arg Trp Glu Thr Glu Pro Leu
 450 455 460
 Met Asn Leu Gly Asn Ala Leu Asp Leu Leu Val Thr Ser Ala Ala Trp
 465 470 475 480
 Thr Ala Gly Glu Gln Val Leu Lys Lys Thr Phe Leu Ser Gln Leu Leu
 485 490 495
 Thr Ala Val Ala Leu Pro Leu Gly Leu Leu Lys Val Ala Arg Val Val
 500 505 510
 Asp Asn Pro Phe Ser Val Ala Lys Ala Arg Ala Asp Lys Ala Gly Glu
 515 520 525
 Val Leu Ala Asp Ala Leu Ile Ser Lys Val Gln Gly Glu Arg Pro Val
 530 535 540
 Thr Leu Ile Gly Tyr Ser Leu Gly Ser Arg Val Ile Phe Ala Cys Leu
 545 550 555 560
 Gln Ser Leu Ala Lys Arg Arg Ala Phe Gly Leu Val Glu Ser Ala Ile
 565 570 575
 Leu Met Gly Ala Pro Thr Pro Ser Asn Ser Glu Gln Trp Cys Arg Ile
 580 585 590
 Arg Ser Val Val Ser Gly Arg Leu Val Asn Val Tyr Ser Glu Asn Asp
 595 600 605
 Ser Val Leu Ala Leu Leu Tyr Arg Thr Ser Ser Leu Gln Leu Gly Val
 610 615 620
 Ala Gly Leu Gln Pro Val Glu Gly Val Ser Gly Val Glu Asn Leu Asp
 625 630 635 640
 Val Ser Asp Leu Ile Ser Gly His Leu Arg Tyr Gln Phe Leu Val Gly
 645 650 655
 Arg Ile Leu Ser Val Val Gly Leu Glu Ser Ile Asp Ala Arg Glu Val
 660 665 670
 Ala Leu Glu Glu Ala Ala Leu Glu Ala Lys Asp Arg Arg Gln Glu Gln
 675 680 685
 Glu Arg Ala His Asn Glu Arg Gln Ala Gly Phe Met Gly Glu Gly Arg
 690 695 700
 Ser Pro Ser Gln Arg Leu Glu Ser Gln Glu Asp Leu Gln Gly Glu Glu
 705 710 715 720
 Asp Arg Leu Gln Lys Glu Met Gly Lys Ala Arg Val Arg His Ser
 725 730 735

<210> 46
 <211> 510
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 46
 atggccgata tcgatgtcaa ggttgctcaa tggaagcttg ttgaggttg ccgtgttg 60
 ctgatccgca gcggtcctta caccggcaag cttgctgcca ttgtcgagat catcgaccac 120
 aagcgtgtac gtttttcaac ggagaaattc tgagcgcagg acggaaagat catggtcgga 180
 tgtgatattg acaaagaggc gcgatcatag gtcctgggtg acggtccttc caccgaggag 240
 aacaagatcg ttccccgtca cgctcttctt ctcgctcacg ccactctcac ccccttcgtc 300
 attcccaaac tccccgcgc tgccggcact ggccccgtca agaagctctg ggagaagaac 360
 gagatcgatg gaaagtgggc taagagcacc attgtcaga agactgagcg cgctgagcgg 420
 aggaagaacc ttaccgactt cgagcgcttc aaggctccta gactcaagaa gcagggtacgt 480
 tcagtttgcg aaactatggg agaattgtga 510

<210> 47
 <211> 423
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 47
 atggccgata tcgatgtcaa ggttgctcaa tggaagcttg ttgaggttg ccgtgttg 60
 ctgatccgca gcggtcctta caccggcaag cttgctgcca ttgtcgagat catcgaccac 120
 aagcgtgtcc tggttgacgg tccttccacc gaggagaaca agatcgttcc cgtcacgct 180
 cttcctctcg ctcacgccac tctcaccctt ttcgtcattc ccaaactccc ccgcgctgcc 240
 ggcaactggcc ccgtcaagaa gctctgggag aagaacgaga tcgatggaaa gtgggctaag 300
 agcaccattg ctcagaagac tgagcgcgct gagcggagga agaaccttac cgacttcgag 360
 cgcttcaagg tcctcagact caagaagcag gtacgttcag tttgcgaaac tatgggagaa 420
 ttg 423

<210> 48
 <211> 141
 <212> PRT
 <213> *Aspergillus fumigatus*

<400> 48
 Met Ala Asp Ile Asp Val Lys Val Ala Gln Trp Lys Leu Val Glu Val
 1 5 10 15
 Gly Arg Val Val Leu Ile Arg Ser Gly Pro Tyr Thr Gly Lys Leu Ala
 20 25 30
 Ala Ile Val Glu Ile Ile Asp His Lys Arg Val Leu Val Asp Gly Pro
 35 40 45
 Ser Thr Glu Glu Asn Lys Ile Val Pro Arg His Ala Leu Pro Leu Ala
 50 55 60
 His Ala Thr Leu Thr Pro Phe Val Ile Pro Lys Leu Pro Arg Ala Ala
 65 70 75 80
 Gly Thr Gly Pro Val Lys Lys Leu Trp Glu Lys Asn Glu Ile Asp Gly
 85 90 95
 Lys Trp Ala Lys Ser Thr Ile Ala Gln Lys Thr Glu Arg Ala Glu Arg
 100 105 110

Arg Lys Asn Leu Thr Asp Phe Glu Arg Phe Lys Val Leu Arg Leu Lys
 115 120 125

Lys Gln Val Arg Ser Val Cys Glu Thr Met Gly Glu Leu
 130 135 140

<210> 49

<211> 1413

<212> DNA

<213> *Aspergillus fumigatus*

<400> 49

```

atggctctcc gccggccatt aacacttccg aggcacattc tcaatggagc ttgttttaggc 60
ttgcgaccag ctgtgtctcg cgccgctctg gcttatgggc aggagcagag gaaagggctt 120
gcaacagcag ttcccccggt cactcaaaat gcggctgggt ccaaaggccc cacggcaatg 180
gtcttctctca acatgggtgg gccatcgaag attgacgaag tggaagattt tctgagcaga 240
ttatttggtat gcatttctca atatgccga tgctaccacc atgtatgagt ctgacaaact 300
ctctcttctct ataccaggcc gatggcgatc tgatttctct cggacgactt caatcatacc 360
tcggccctct catcgctaag cgcagaaccc caaagatcca acggcaatac tcggatattg 420
gtggagggtc accgatcagg aaatgggtcc agtatcagtg cgaggaaatg tgcagattgc 480
tagacaaaat caatcccga acggctcctc acaagcctta cgtcgcgttc cggtagcccg 540
accctctgac ggaagaaatg tacacaaagt tgctggaaga tggattcggc aacgggaaag 600
gcgggcgcgc tgtcgcgttc acacagtacc cccaatattc gtgctccacc acgggtagct 660
cgctgaacga gttgtggaag tggagaacca ggcttgaggg taagcgtgca aatggcaaca 720
tggaccccg cgttgccatc cagtggagtg tcattgatcg atggccaacg caccctggcc 780
tcgtggaggc ttctgcccgg aacattgagg agcagctgaa gacataccca gaggagaagc 840
gaaacggtgt cgttctcttg ttctcagccc acagtctgcc catgagtgtt gtcaacagag 900
gtgagactca tcttcttacc gaacaacaag atttgctcgc taacacattt cctaggcgac 960
ccatattctg ctgaagtgtg tgcaactgtg catgctgtca tgcaaagatt gaatttcagc 1020
aatccttacc gactgtgctg gcagtcctaa gtgggaccgt cagcttggct tggagcccaa 1080
actagcgata cggtcgaaaa ctatgtcaaa cgtggacaga ccgatattat tctagttccc 1140
attgccttca ccagcgacca tattgagact ctgtacgagt tggatctgga agtgataaag 1200
gaagcaaat ccccgggagt caagagagcc gagagtttga atggtaacct cattttcatt 1260
caggcattag cagacattgc ccaagagcac ctccgtaagg gagagaagtg ctactacag 1320
atgactctgc gctgtcaagg ctgtaagagc gaacggtgcc tggaacagaa gaaattcttt 1380
gctggcgacc gattttcttc tctttagttag tag 1413

```

<210> 50

<211> 1284

<212> DNA

<213> *Aspergillus fumigatus*

<400> 50

```

atggctctcc gccggccatt aacacttccg aggcacattc tcaatggagc ttgttttaggc 60
ttgcgaccag ctgtgtctcg cgccgctctg gcttatgggc aggagcagag gaaagggctt 120
gcaacagcag ttcccccggt cactcaaaat gcggctgggt ccaaaggccc cacggcaatg 180
gtcttctctca acatgggtgg gccatcgaag attgacgaag tggaagattt tctgagcaga 240
ttatttgccg atggcgatct gatttctctc ggacgacttc aatcatacct cggccctctc 300
atcgctaagc gcagaacccc aaagatccaa cggcaatact cggatattgg tggagggtca 360
ccgatcagga aatgggtccga gtatcagtg gcaggaaatgt gcagattgct agacaaaatc 420
aatcccgaaa cggctcctca caagccttac gtcgcgttcc ggtacgccga ccctctgacg 480
gaagaaatgt acacaaagtt gctggaagat ggattcggca acgggaaagg cgggcgcgct 540
gtcgcgttca cacagtaccc ccaatattcg tgctccacca cgggtagctc gctgaacgag 600
ttgtggaagt ggagaaccag gcttgagggt aagcgtgcaa atggcaacat ggaccccgct 660
ggtgccatcc agtggagtgt cattgatcga tggccaacgc accctggcct cgtggaggct 720
ttcggccgga acattgagga gcagctgaag acatacccag aggagaagcg aaacggtgtc 780
gttctcttgt tctcagccca cagtctgccc atgagtgttg tcaacagagg cgacccatat 840

```



```

cctgctgaag ttgctgcaac tgtgcatgct gtcatgcaaa gattgaattt cagcaatcct 900
taccgactgt gctggcagtc ccaagtggga ccgtcagctt ggcttggagc ccaaactagc 960
gatacggtcg aaaactatgt caaacgtgga cagaccgata ttattctagt tcccattgcc 1020
ttcaccagcg accatattga gactctgtac gagttggatc tggaagtgat aaaggaagca 1080
aactccccgg gagtcaagag agccgagagt ttgaatggta accccatttt cattcaggca 1140
ttagcagaca ttgcccaaga gcacctccgt aagggagaga agtgctcact acagatgact 1200
ctgcgctgtc aaggctgtaa gagcgaacgg tgcctggaac agaagaaatt ctttgctggc 1260
gaccgatttt cttctcttgt agtt                                     1284

```

<210> 51

<211> 428

<212> PRT

<213> *Aspergillus fumigatus*

<400> 51

```

Met Ala Leu Arg Arg Pro Leu Thr Leu Pro Arg His Ile Leu Asn Gly
  1              5              10              15

Ala Cys Leu Gly Leu Arg Pro Ala Val Ser Arg Ala Ala Leu Ala Tyr
      20              25              30

Gly Gln Glu Gln Arg Lys Gly Leu Ala Thr Ala Val Pro Pro Val Thr
      35              40              45

Gln Asn Ala Ala Gly Ser Lys Gly Pro Thr Ala Met Val Phe Leu Asn
      50              55              60

Met Gly Gly Pro Ser Lys Ile Asp Glu Val Glu Asp Phe Leu Ser Arg
      65              70              75              80

Leu Phe Ala Asp Gly Asp Leu Ile Pro Leu Gly Arg Leu Gln Ser Tyr
      85              90              95

Leu Gly Pro Leu Ile Ala Lys Arg Arg Thr Pro Lys Ile Gln Arg Gln
      100             105             110

Tyr Ser Asp Ile Gly Gly Gly Ser Pro Ile Arg Lys Trp Ser Glu Tyr
      115             120             125

Gln Cys Glu Glu Met Cys Arg Leu Leu Asp Lys Ile Asn Pro Glu Thr
      130             135             140

Ala Pro His Lys Pro Tyr Val Ala Phe Arg Tyr Ala Asp Pro Leu Thr
      145             150             155             160

Glu Glu Met Tyr Thr Lys Leu Leu Glu Asp Gly Phe Gly Asn Gly Lys
      165             170             175

Gly Gly Arg Ala Val Ala Phe Thr Gln Tyr Pro Gln Tyr Ser Cys Ser
      180             185             190

Thr Thr Gly Ser Ser Leu Asn Glu Leu Trp Lys Trp Arg Thr Arg Leu
      195             200             205

Glu Gly Lys Arg Ala Asn Gly Asn Met Asp Pro Ala Gly Ala Ile Gln
      210             215             220

Trp Ser Val Ile Asp Arg Trp Pro Thr His Pro Gly Leu Val Glu Ala
      225             230             235             240

```

Phe Ala Arg Asn Ile Glu Glu Gln Leu Lys Thr Tyr Pro Glu Glu Lys
 245 250 255
 Arg Asn Gly Val Val Leu Leu Phe Ser Ala His Ser Leu Pro Met Ser
 260 265 270
 Val Val Asn Arg Gly Asp Pro Tyr Pro Ala Glu Val Ala Ala Thr Val
 275 280 285
 His Ala Val Met Gln Arg Leu Asn Phe Ser Asn Pro Tyr Arg Leu Cys
 290 295 300
 Trp Gln Ser Gln Val Gly Pro Ser Ala Trp Leu Gly Ala Gln Thr Ser
 305 310 315 320
 Asp Thr Val Glu Asn Tyr Val Lys Arg Gly Gln Thr Asp Ile Ile Leu
 325 330 335
 Val Pro Ile Ala Phe Thr Ser Asp His Ile Glu Thr Leu Tyr Glu Leu
 340 345 350
 Asp Leu Glu Val Ile Lys Glu Ala Asn Ser Pro Gly Val Lys Arg Ala
 355 360 365
 Glu Ser Leu Asn Gly Asn Pro Ile Phe Ile Gln Ala Leu Ala Asp Ile
 370 375 380
 Ala Gln Glu His Leu Arg Lys Gly Glu Lys Cys Ser Leu Gln Met Thr
 385 390 395 400
 Leu Arg Cys Gln Gly Cys Lys Ser Glu Arg Cys Leu Glu Gln Lys Lys
 405 410 415
 Phe Phe Ala Gly Asp Arg Phe Ser Ser Leu Val Val
 420 425

<210> 52

<211> 1536

<212> DNA

<213> *Aspergillus fumigatus*

<400> 52

atgatttatac tccgggtcctc gttgctgagg tctggattgg ctcgagatcc tgctcgccctg 60
 tgttcacaat gcttctcacg actctcacca tcacgacgac ctgtcgagcagc tcgcagcttc 120
 ttctcctcat ctccggctgcg ggctggcatt gccgatcatg aatcaactcc ctgcactgtc 180
 caaaagacct atttttctgc caatcggacc gcagatggct tacttgcatc cttatccgcc 240
 gtcaatagct cccctcgaag tattgccgac aatgcgttat cacaggggtgc agccagttcg 300
 gagtcgatta cttcacagtc tacttcacaa gagttacctc atcgccggag gaagcgggta 360
 aaggaagagg cggccaagaa taatgctgca gaaaccgaac tccctcctga tgccctcgtc 420
 caattgtcca ccctctcatc agccctccct gcgacttccc tgcgcgcgcaa gctggctgcg 480
 tttctcgccc tcacaaaagcc tcgtctctcg ttcttgatcg tggtgacgac tacctccgct 540
 tatgggatgt acccgatctc ctctcttctc acacttgacc cttcaatgac tcccctaccg 600
 accctctcga cctcaacctt gacctttctc tacctgacca caggaaacct cttgtcttca 660
 tgcagcgcca ataccttgaa tatgctcctt gaacctaaat acgatgccct catgtcacgg 720
 acacggaacc ggccgttagt gcgggggcta ctctcacgcc gtgctgcggg attgtttgcg 780
 attgcgactg ctgctgcagg tctcggtttg ttatacattg gaacgaaccc tacgactact 840
 gcgctctccg ccagtaatat ctgtctctat gcctttgtgt atacgccgct gaagcgtata 900
 tcagtgatca acacctgggt aggcgcctgt gtaggaggca ttctccggtt gatgggttgg 960
 accgctgcag caggccagac agcgaccact ggccacgaca gctggcgagg catgttgttc 1020

```

agcaaggata gcatcggtgg ttggctcctg ggtggcattc tctttgcatg gcagtttcct 1080
catttcaatg ctttgtccta catgatccgt gaagagtaca aggcagccgg gtacaggatg 1140
ctcgcgatgga ctaatcccgc cgcaaagtcg cgtgtcgcac tacgatattc tcttctcatg 1200
tttcctttct ccgtcggtct ctggtgggta ggagtgtgct gtaatggttt cctgggttga 1260
agcacggcgg ccaatggctg gctagtcaaa gaggcctaca aattctggcg gcaccaaggc 1320
gccaacggca gtgctcgacg cctcttctgg gccagtattt ggcagctgcc aatcctcctt 1380
gtcgggtggtc tggtcacgaa gaaaggtctc tgggatgggt tctggaacaa tgttttcggt 1440
cagcctgtgg aagacgagga tgactatctc tgggaggatg aggatgaagt ggcagaggcg 1500
gagcgcaaga tgatacctgc gaagacgagt agctcg 1536

```

<210> 53

<211> 1536

<212> DNA

<213> *Aspergillus fumigatus*

<400> 53

```

atgatttata tccggtcctc gttgctgagg tctggattgg ctcgagatcc tgctcgccctg 60
tgttcacaat gcttctcacg actctcacca tcacgacgac ctgtcgagct tcgcagcttc 120
ttctcctcat ctcggtcgcg ggctggcatt gccgatcatg aatcaactcc ctcgactgtc 180
caaaagacat atttttctgc caatcggacc gcagatggct tacttgcatc cttatccgcc 240
gtcaatagct cccctcgaa gattgccgac aatgcgttat cacagggtgc agccagttcg 300
gagtcgatta cttcacagtc tacttcacaa gagttacctc atcgccggag gaagcgggta 360
aaggaagagg cggccaagaa taatgctgca gaaaccgaac tccctcctga tgcctcgtct 420
caattgtcca ccctctcatc agccctccct gcgacttccc tgcgcgcgaa gctggctgcg 480
tttctcgccc tcacaaagcc tcgtctctcg ttcttgatcg tgttgacgac tacctccgct 540
tatgggatgt acccgatctc ctctcttctc acacttgacc cttcaatgac tcccctaccg 600
accctctcga cctcaacctt gacctttctc taactgacca caggaacctt cttgtcttca 660
tgcagcgcca ataccttgaa tatgctcctt gaacctaaat acgatgccct catgtcacgg 720
acacggaacc ggccgttagt gcgggggcta ctctcacgcc gtgctgcggg attggttgcg 780
attgcgactg ctgctgcagg tctcggtttg ttatacattg gaacgaacc tacgactact 840
gcgctctccg ccagtaatat ctgtctctat gcctttgtgt atacgccgct gaagcgtata 900
tcagtgatca acacctgggt aggcgccgtg gtaggaggca ttctccggt gatgggttg 960
accgctgcag caggccagac agcgaccact ggccacgaca gctggcgagg catgttggtc 1020
agcaaggata gcatcggtgg ttggctcctg ggtggcattc tctttgcatg gcagtttcct 1080
catttcaatg ctttgtccta catgatccgt gaagagtaca aggcagccgg gtacaggatg 1140
ctcgcgatgga ctaatcccgc cgcaaagtcg cgtgtcgcac tacgatattc tcttctcatg 1200
tttcctttct ccgtcggtct ctggtgggta ggagtgtgct gtaatggttt cctgggttga 1260
agcacggcgg ccaatggctg gctagtcaaa gaggcctaca aattctggcg gcaccaaggc 1320
gccaacggca gtgctcgacg cctcttctgg gccagtattt ggcagctgcc aatcctcctt 1380
gtcgggtggtc tggtcacgaa gaaaggtctc tgggatgggt tctggaacaa tgttttcggt 1440
cagcctgtgg aagacgagga tgactatctc tgggaggatg aggatgaagt ggcagaggcg 1500
gagcgcaaga tgatacctgc gaagacgagt agctcg 1536

```

<210> 54

<211> 512

<212> PRT

<213> *Aspergillus fumigatus*

<400> 54

```

Met Ile Tyr Leu Arg Ser Ser Leu Leu Arg Ser Gly Leu Ala Arg Asp
  1             5             10             15

```

```

Pro Ala Arg Leu Cys Ser Gln Cys Phe Ser Arg Leu Ser Pro Ser Arg
      20             25             30

```

```

Arg Pro Val Ala Val Arg Ser Phe Phe Ser Ser Ser Arg Leu Arg Ala
      35             40             45

```

```

Gly Ile Ala Asp His Glu Ser Thr Pro Ser Thr Val Gln Lys Thr Tyr

```

50	55	60
Phe Ser Ala Asn Arg Thr Ala Asp Gly Leu Leu Ala Ser Leu Ser Ala 65 70 75 80		
Val Asn Ser Ser Pro Arg Ser Ile Ala Asp Asn Ala Leu Ser Gln Gly 85 90 95		
Ala Ala Ser Ser Glu Ser Ile Thr Ser Gln Ser Thr Ser Gln Glu Leu 100 105 110		
Pro His Arg Arg Arg Lys Arg Leu Lys Glu Glu Ala Ala Lys Asn Asn 115 120 125		
Ala Ala Glu Thr Glu Leu Pro Pro Asp Ala Ser Ser Gln Leu Ser Thr 130 135 140		
Leu Ser Ser Ala Leu Pro Ala Thr Ser Leu Arg Arg Lys Leu Ala Ala 145 150 155 160		
Phe Leu Ala Leu Thr Lys Pro Arg Leu Ser Phe Leu Ile Val Leu Thr 165 170 175		
Thr Thr Ser Ala Tyr Gly Met Tyr Pro Ile Ser Ser Leu Leu Thr Leu 180 185 190		
Asp Pro Ser Met Thr Pro Leu Pro Thr Leu Ser Thr Ser Thr Leu Thr 195 200 205		
Phe Leu Tyr Leu Thr Thr Gly Thr Phe Leu Ser Ser Cys Ser Ala Asn 210 215 220		
Thr Leu Asn Met Leu Leu Glu Pro Lys Tyr Asp Ala Leu Met Ser Arg 225 230 235 240		
Thr Arg Asn Arg Pro Leu Val Arg Gly Leu Leu Ser Arg Arg Ala Ala 245 250 255		
Val Leu Phe Ala Ile Ala Thr Ala Ala Ala Gly Leu Gly Leu Leu Tyr 260 265 270		
Ile Gly Thr Asn Pro Thr Thr Thr Ala Leu Ser Ala Ser Asn Ile Cys 275 280 285		
Leu Tyr Ala Phe Val Tyr Thr Pro Leu Lys Arg Ile Ser Val Ile Asn 290 295 300		
Thr Trp Val Gly Ala Val Val Gly Gly Ile Pro Pro Leu Met Gly Trp 305 310 315 320		
Thr Ala Ala Ala Gly Gln Thr Ala Thr Thr Gly His Asp Ser Trp Arg 325 330 335		
Asp Met Leu Phe Ser Lys Asp Ser Ile Gly Gly Trp Leu Leu Gly Gly 340 345 350		
Ile Leu Phe Ala Trp Gln Phe Pro His Phe Asn Ala Leu Ser Tyr Met 355 360 365		
Ile Arg Glu Glu Tyr Lys Ala Ala Gly Tyr Arg Met Leu Ala Trp Thr 370 375 380		

Asn Pro Ala Ala Asn Ala Arg Val Ala Leu Arg Tyr Ser Leu Leu Met
 385 390 395 400
 Phe Pro Phe Ser Val Gly Leu Trp Trp Val Gly Val Val Gly Asn Gly
 405 410 415
 Phe Leu Val Gly Ser Thr Ala Ala Asn Gly Trp Leu Val Lys Glu Ala
 420 425 430
 Tyr Lys Phe Trp Arg His Gln Gly Ala Asn Gly Ser Ala Arg Arg Leu
 435 440 445
 Phe Trp Ala Ser Ile Trp Gln Leu Pro Ile Leu Leu Val Gly Gly Leu
 450 455 460
 Val Thr Lys Lys Gly Leu Trp Asp Gly Val Trp Asn Asn Val Phe Gly
 465 470 475 480
 Gln Pro Val Glu Asp Glu Asp Asp Tyr Leu Trp Glu Asp Glu Asp Glu
 485 490 495
 Val Ala Glu Ala Glu Arg Lys Met Ile Pro Ala Lys Thr Ser Ser Ser
 500 505 510

<210> 55

<211> 1626

<212> DNA

<213> *Aspergillus fumigatus*

<400> 55

atgctcaacg ccgcggttgc tgccccgcga tgttttgtat atcccactga tcgcgcagca 60
 atgcgcttgg gctttgctct tcgtctctcc tctcctgcac ctctcttctc aacagcacct 120
 ttccgtcgac agttgcatgc ttccggcgctc cgatcaattg aacctgttat ctttcgaaat 180
 agccttgaaa agactcttga ggctcatcga tcttccaatc gagccagtct gatccgcaag 240
 gtgattaacc acgattgtcc tgctgaaacg cccctccaa ttttaccact tgagaatcgt 300
 gctggctcatg atcaatcatc tcaaaaggcc tcttccgtgt caaatgcaga gtcagagtcc 360
 ccccggtctt ctgcgctctgc gagacgagcg cagaggaagg cccgttcgcc cagccaagta 420
 gccaccccg cgcgcctcga cgcggagatc cgcgctcttg agctctacat gacaccgacc 480
 aagggccgac cggcacaaag tccttggttg aagtacttga ctaccgattg gaaaacgccc 540
 gatgccgttt cgcgtctcga cgcggagatc cgcgctcttg agctctacat gacaccgacc 600
 ccgtcggagc ggactgagat agatcggctg gttgcagata tgggtaggtt gctagcggga 660
 atcgtcccca gccgcgcca ggtaaccggt tcatggcgga cgcgatttgc cttgagccac 720
 tcgggtctcg attttgtctt acctgtcccg gattcagacc gatccacccg tgacgttcgc 780
 aagccgagtg ccacacggcc caaggtgtct cagacttaca aaaagctctt acatgaagtg 840
 ggacatgcgc ttcagcagtc cccctcgttc gcgagcgag tccgcatcat aggcagccgt 900
 ttccccgtcc tctcagccat ccatcgcccc acgggcccgc tgctgcagtt cactgcggt 960
 gaagggctac cggcctctgt cgaataacat atggattacc aggccgagta tccctcgatc 1020
 cggccgctct acgtgaccgc tcgcctgatc ctggaggcgc ggggtaggta tggccgtact 1080
 cagatgtcta ttgaatccga tgccctcgta atgcttctcg tggccttcct caaatgaac 1140
 cacggcggtt ttcagcgcc cgactgtctc ggcgagcagc tgatcgcggt tctgcgcgcc 1200
 tacggcagcg atattgacct gaccaccacc ggtgtgtccg tcgatcccc cagttgggtc 1260
 aatgctagta cgggtcaaacg cgccagcgcc ctgtacgcgc ccgatgatct acccgcgcat 1320
 ctgcgcggcc agcgtctcct catcagcctc aagagaacag cagccgccag acgcaatctg 1380
 cctgccgcca gccggctgtg cgtgcaggac cccaccaatt acatgaatga tctggggccg 1440
 agctgcgtgc gtacgttgga actccagcac acgttctcgc ttgctcatga ccgtctcggc 1500

```

gcaagtctca agcgctggga tgacagtga cgggccgcga acgttagtat cctgacacgg 1560
gccctgcaag caaacttttc tgattttgaa aatctacgcg ccaaatcgct taagctcaac 1620
gcgacc                                     1626

```

<210> 56

<211> 1626

<212> DNA

<213> *Aspergillus fumigatus*

<400> 56

```

atgctcaacg ccgcggttgc tgccccgcga tgttttgtat atcccactga tcgcgcagca 60
atgcgcttgg gctttgctct tcgtctctcc tctcctgcac ctctcttctc aacagcacct 120
ttccgtcgac agttgcatgc ttccggcgtc cgatcaattg aacctgttat ctttcgaaat 180
agccttgaaa agactcttga ggctcatcga tctccaatc gagccagtct gatccgcaag 240
gtgattaacc acgattgtcc tgctgaaacg cccctccaa ttttaccact tgagaatcgt 300
gctggctcatg atcaatcatc tcaaaaggcc tctccgtgt caaatgcaga gtcagagtcc 360
ccccggtctt ctgcgcctgc gagacgagcg cagaggaagg cccgttcgcc cagccaagta 420
gccacccgcg agccccagac aacagaatat ccacaactgc aatggcatgc agatgaaacc 480
aagggccgac cggcacaaag tccttggtcg aagtactga ctaccgattg gaaaacgccc 540
gatgccgttt cgcgtctcga cgcggagatc cgcgctcttg agctctacat gacaccgacc 600
ccgtcggagc ggactgagat agatcggctg gttgcagata tgggtagggt gctagcggga 660
atcgteccca gccgcgccca ggtaaccggt tcatggcgga cgcgatttgc cttgagccac 720
tcgggtctcg attttgtctt acctgtcccg gattcagacc gatccacccg tgacgttcgc 780
aagccgagtg ccacacggcc caaggtgctc cagacttaca aaaagctctt acatgaagtg 840
ggacatgcgc ttcagcagtc cccctcgttc gcggagcgag tccgcatcat aggcagccgt 900
ttccccgtcc tctcagccat ccacgcgcc acgggcccgc tgctgcagtt ccaactgcgtt 960
gaagggtac cggcctctgt cgaatacatc atggattacc aggccgagta tccctcgatc 1020
cggccgctct acgtgaccgc tcgcctgatc ctggaggcgc ggggtaggta tggccgtact 1080
cagatgtcta ttgaatccga tgccctcgta atgcttctcg tggccttctt caaaatgaac 1140
cacggcggtt ttcagcggcc cgactgtctc ggcgagcagc tgatcgcgtt tctgcgcgcc 1200
tacggcagcg atattgacct gaccaccacc ggtgtgtccg tcgatcccc cagttgggtc 1260
aatgctagta cgggtcaaac cgccagcgcc ctgtacgcgc ccgatgatct acccgcgcac 1320
ctgcgcggcc agcgtccct catcagcctc aagagaacag cagccgccag acgcaatctg 1380
cctgcgcgca gccggctgtg cgtgcaggac cccaccaatt acatgaatga tctgggcccgc 1440
agctgcgtgc gtacgttgga actccagcac acgttctcgc ttgctcatga ccgtctcggc 1500
gcaagtctca agcgctggga tgacagtga cggccgcga acgttagtat cctgacacgg 1560
gccctgcaag caaacttttc tgattttgaa aatctacgcg ccaaatcgct taagctcaac 1620
gcgacc                                     1626

```

<210> 57

<211> 542

<212> PRT

<213> *Aspergillus fumigatus*

<400> 57

```

Met Leu Asn Ala Ala Val Ala Ala Pro Arg Cys Phe Val Tyr Pro Thr
 1             5             10             15

Asp Arg Ala Ala Met Arg Leu Gly Phe Ala Leu Arg Leu Ser Ser Pro
      20             25             30

Ala Pro Leu Phe Ser Thr Ala Pro Phe Arg Arg Gln Leu His Ala Ser
      35             40             45

Gly Val Arg Ser Ile Glu Pro Val Ile Phe Arg Asn Ser Leu Glu Lys
      50             55             60

Thr Leu Glu Ala His Arg Ser Ser Asn Arg Ala Ser Leu Ile Arg Lys
      65             70             75             80

```

Val Ile Asn His Asp Cys Pro Ala Glu Thr Pro Pro Pro Ile Leu Pro
 85 90 95
 Leu Glu Asn Arg Ala Gly His Asp Gln Ser Ser Gln Lys Ala Ser Ser
 100 105 110
 Val Ser Asn Ala Glu Ser Glu Ser Pro Arg Ser Ser Ala Pro Ala Arg
 115 120 125
 Arg Ala Gln Arg Lys Ala Arg Ser Pro Ser Gln Val Ala Thr Pro Gln
 130 135 140
 Pro Gln Thr Thr Glu Tyr Pro Gln Leu Gln Trp His Ala Asp Glu Thr
 145 150 155 160
 Lys Gly Arg Pro Ala Gln Ser Pro Trp Leu Lys Tyr Leu Thr Thr Asp
 165 170 175
 Trp Lys Thr Pro Asp Ala Val Ser Arg Leu Asp Ala Glu Ile Arg Ala
 180 185 190
 Leu Glu Leu Tyr Met Thr Pro Thr Pro Ser Glu Arg Thr Glu Ile Asp
 195 200 205
 Arg Leu Val Ala Asp Met Gly Arg Leu Leu Ala Gly Ile Val Pro Ser
 210 215 220
 Pro Pro Gln Val Thr Gly Ser Trp Arg Thr Arg Phe Ala Leu Ser His
 225 230 235 240
 Ser Gly Leu Asp Phe Val Leu Pro Val Pro Asp Ser Asp Arg Ser Thr
 245 250 255
 Arg Asp Val Arg Lys Pro Ser Ala Thr Arg Pro Lys Val Leu Gln Thr
 260 265 270
 Tyr Lys Lys Leu Leu His Glu Val Gly His Ala Leu Gln Gln Ser Pro
 275 280 285
 Ser Phe Ala Glu Arg Val Arg Ile Ile Gly Ser Arg Phe Pro Val Leu
 290 295 300
 Ser Ala Ile His Arg Pro Thr Gly Arg Leu Leu Gln Phe His Cys Gly
 305 310 315 320
 Glu Gly Leu Pro Ala Ser Val Glu Tyr Ile Met Asp Tyr Gln Ala Glu
 325 330 335
 Tyr Pro Ser Ile Arg Pro Leu Tyr Val Thr Ala Arg Leu Ile Leu Glu
 340 345 350
 Ala Arg Gly Arg Tyr Gly Arg Thr Gln Met Ser Ile Glu Ser Asp Ala
 355 360 365
 Leu Val Met Leu Leu Val Ala Phe Leu Lys Met Asn His Gly Arg Phe
 370 375 380
 Gln Arg Pro Asp Cys Leu Gly Glu Gln Leu Ile Ala Phe Leu Arg Ala
 385 390 395 400

Tyr Gly Ser Asp Ile Asp Leu Thr Thr Thr Gly Val Ser Val Asp Pro
 405 410 415
 Pro Ser Trp Phe Asn Ala Ser Thr Val Lys Arg Ala Ser Ala Leu Tyr
 420 425 430
 Ala Pro Asp Asp Leu Pro Ala His Leu Arg Gly Gln Arg Ser Leu Ile
 435 440 445
 Ser Leu Lys Arg Thr Ala Ala Ala Arg Arg Asn Leu Pro Ala Ala Ser
 450 455 460
 Arg Leu Cys Val Gln Asp Pro Thr Asn Tyr Met Asn Asp Leu Gly Arg
 465 470 475 480
 Ser Cys Val Arg Thr Leu Glu Leu Gln His Thr Phe Ser Leu Ala His
 485 490 495
 Asp Arg Leu Gly Ala Ser Leu Lys Arg Trp Asp Asp Ser Glu Pro Ala
 500 505 510
 Ala Asn Val Ser Ile Leu Thr Arg Ala Leu Gln Ala Asn Phe Ser Asp
 515 520 525
 Phe Glu Asn Leu Arg Ala Lys Ser Leu Lys Leu Asn Ala Thr
 530 535 540

<210> 58

<211> 2356

<212> DNA

<213> *Aspergillus fumigatus*

<400> 58

```

atgggggttg aggatccgcg gcgagcagtc caggcagagt cgtatctgga gactaccgcg 60
tcgcagctcg tcgatgcgct tatatcacgg cogaatcttg agagtggctt gggtcgaagg 120
aattttgttc ctctaggca ggtcccgggt gtgcagcca tggagcggac gaaaaatgct 180
atacaatcaa ataattccag ctgcggggcg caactttcgg atgcattacc cgagagcgag 240
aaatcacaga gtgcagggca ggttattgtc ccgacacgga tgcaggaact tctcgaccgc 300
ggtcgtccca ttgaggcggc ccaatttttt ctggagacac atgccgcttc attgaaaggc 360
atattcctcag acaggaagga aatggctacg aaggatttct tcgtcaactg caaagaggac 420
aatgtgttta ttgccagaag tgtgtttgag cggttggaag aggtggatag aatcacgcct 480
gagatgtgga agacgttgat gctggctttg gcgaagaaag ggtgcattga atcagttgcg 540
agtgtttata cgcgatacat gcgcaagttc ccttgccctc cggagatggt cgacgttggt 600
ctgcggagtt tgcttgaatc ccaccgactc accactgcga aatggttcct cttgcgcaat 660
ctacaacatg accgtgattg cggtttggtc ggagcctacc tctccggcct gtggcggaag 720
acaagaagca tcgagttatt gaacgggcag ttgaaaaaga tattgaccat tcttccaaag 780
ttcgaanaac aacctagcga caaactattt aaccgggtga tcaaggcata tggtgaattt 840
gggcgggttg ccgatgccga agctctggtg catgatatga ccactttata tgggatccct 900
cttcgttgcc gaactcaggg cctattggta tacgccaaag ctctgaactg tgactgggag 960
ggagttgacg caggactgca agagatgcac aaactcaagc tgacgagacg ccggcgagac 1020
ttccttccta tttttgatcg aatattttct gagtactggg tctcacattc gggaattgag 1080
attcgcaatt ttgtgttccg gtaccttgat aaattcgaca ttgtccccga tcgcgtgctc 1140
tacaagcaca ctttgaggcg tttcgtggag aaaggagaca aggaaatgat tgctgaattt 1200
acaagtatgg cgaagcagcg atcgtggaat atccccataa acgagcagca attcttgag 1260
atactacggt ctgcgtgcct cgcattggaa ggagcaccag tggggttctg gcaaattgctg 1320
caggcagcgc gtgtcaagta cgggcacagc tccacgtctc agcgtatcat gggctacgac 1380
caacagtcac tccctttgcc ggaagtcaac agcatgccat atacacagaa tccgctatcg 1440
tggtaccaga gaacgatgca agagaccacg ccgtcgaagc ctgtcgacca atatcagaaa 1500
ctccataagc agatgacca ttttctgcac gctggaaagc tgaaggaagc attgaagtgc 1560

```



```

tttcaaaatg ctaaaaatgc cgggttccag atgaggcagc ttcacgttga attggcggtc 1620
atagcgactt tgcttgagga cggccttagt gcagcgcgca gtctcatcga gtctgaatgg 1680
cggactatcc gtcaccttgt ccgcttctct cctatcttct ttcgtcaagt catggcggtc 1740
gacgaggatg cgggtggcca cattgtccag atggcagtc ttcgcttcta ccagctttgt 1800
tggtctacga aacacatgaa ggtcaagcat caccttactg ttgcgacaag ccgtcgcttg 1860
atctcccaac ataagccgga aatggctctg gagcttctga cggccgtgta caagtcccgt 1920
tataggtttg cagcgacctt tgacgggggt tgcataga tggttgcgcg cgccttcgcc 1980
gcgacagaca acattctagg cttacgatgg tgtattctta ctgctttatc acgcgatagt 2040
gcactcaatc atgattttgt ggtggaagt cgccgaatct tgggcactct aagtccacct 2100
tccgcggtgg atgccaccgc cggccccgtc actcatgagc agctggaata cctttattac 2160
atcgccgatc tgctcgagga gaagaatgag ggggtcgccc cgatatggga gctcaagcat 2220
gacgccacac tgaagcagtc ttcgaggcga cagttgaagc aacctcttga cgcaagccgt 2280
cttttcaacc agtccgatgt ccgcgagacc gtcaagcgat gggacgaaga atacgagctg 2340
gaggcagtgc tgggta 2356

```

<210> 59

<211> 2356

<212> DNA

<213> *Aspergillus fumigatus*

<400> 59

```

atgggggttg aggatccgcg gcgagcagtc caggcagagt cgtatctgga gactaccg 60
tcgcagctcg tcgatgcgct tatatcacgg ccgaatcttg agagtggctt gggtcgaagg 120
aattttgttc ctcttaggca ggtcccgggt gtcgacgcca tggagcggac gaaaaatgct 180
atacaatcaa ataattccag ctccgcgggc caactttcgg atgcattacc cgagagcgag 240
aaatcacaga gtgcagggca ggttattgtc ccgacacgga tgcaggaact tctcgaccgc 300
ggtcgtccca ttgaggcggc ccaatttttt ctggagacac atgccgcttc attgaaaggc 360
atatcctcag acaggaagga aatggctacg aaggtattct tcgtcaactg caaagaggac 420
aatgtgttta ttgccagaag tgtgttgag tgtgttggaag aggtggatag aatcacgcct 480
gagatgttga agacgttgat gctggctttg gcgaagaaag ggtgcattga atcagttgcg 540
agtgtttata cgcgatacat gcgcaagttc ccttgccctc cggagatggg cgacgtttgtg 600
ctgcggagtt tgcttgaatc ccaccgactc accactgcga aatggttcct ctgcgcaat 660
ctacaacatg accgtgattg cggtttgtgc ggagccatcc tctccggcct gtggcggaag 720
acaagaagca tcgagttatt gaacgggcag ttgaaaaaga tattgaccat tcttccaaag 780
ttcgaaaaac aacctagcga caaactatth aacctcggtg tcaaggcata tgttgaaatt 840
gggcgggttg ccgatgccga agctctgggt catgatatga ccactttata tgggatccct 900
cttcgttgcc gaactcaggg cctattggta tacgccaagg ctctgaactg tgactgggag 960
ggagttgacg caggactgca agagatgcac aaactcaagc tgacgagacg ccggcgagac 1020
ttccttccta tttttgatcg aatattttct gagtactggg tctcacattc gggaattgag 1080
attcgcaatt ttgtgttccg gtaccttgat aaattcgaca ttgtccccga tcgctgctc 1140
tacaagcaca tcttgagggc tttcgtggag aaaggagaca aggaaatgat tgctgaattt 1200
acaagtatgg cgaagcagcg atcgtggaat atccccataa acgagcagca attcttggag 1260
atactacggt ctctcgccct cgcattggaa ggagcaccag tggggttctg gcaaattgctg 1320
caggcagcgc gtgtcaagta cgggcacagc tccacgtctc agcgtatcat gggctacgac 1380
caacagtcac tccctttgcc ggaagtcaac agcatgccat atacacagaa tccgctatcg 1440
tggtaccaga gaacgatgca agagaccag ccgtcgaaag ctgtcgacca atatcagaaa 1500
ctccataagc agatgaccca ttttctgcac gctggaaaag tgaaggaagc attgaagtgc 1560
tttcaaaatg ctaaaaatgc cgggttccag atgaggcagc ttcacgttga attggcggtc 1620
atagcgactt tgcttgagga cggccttagt gcagcgcgca gtctcatcga gtctgaatgg 1680
cggactatcc gtcaccttgt ccgcttctct cctatcttct ttcgtcaagt catggcggtc 1740
gacgaggatg cgggtggcca cattgtccag atggcagtc ttcgcttcta ccagctttgt 1800
tggtctacga aacacatgaa ggtcaagcat caccttactg ttgcgacaag ccgtcgcttg 1860
atctcccaac ataagccgga aatggctctg gagcttctga cggccgtgta caagtcccgt 1920
tataggtttg cagcgacctt tgacgggggt tgcataga tggttgcgcg cgccttcgcc 1980
gcgacagaca acattctagg cttacgatgg tgtattctta ctgctttatc acgcgatagt 2040
gcactcaatc atgattttgt ggtggaagt cgccgaatct tgggcactct aagtccacct 2100
tccgcggtgg atgccaccgc cggccccgtc actcatgagc agctggaata cctttattac 2160
atcgccgatc tgctcgagga gaagaatgag ggggtcgccc cgatatggga gctcaagcat 2220
gacgccacac tgaagcagtc ttcgaggcga cagttgaagc aacctcttga cgcaagccgt 2280
cttttcaacc agtccgatgt ccgcgagacc gtcaagcgat gggacgaaga atacgagctg 2340

```

gaggcagtgc tgggta

2356

<210> 60

<211> 785

<212> PRT

<213> Aspergillus fumigatus

<400> 60

Met Gly Leu Glu Asp Pro Arg Arg Ala Val Gln Ala Glu Ser Tyr Leu
 1 5 10 15

Glu Thr Thr Arg Ser Gln Leu Val Asp Ala Leu Ile Ser Arg Pro Asn
 20 25 30

Leu Glu Ser Gly Leu Gly Arg Arg Asn Phe Val Pro Pro Arg Gln Val
 35 40 45

Pro Val Val Asp Ala Met Glu Arg Thr Lys Asn Ala Ile Gln Ser Asn
 50 55 60

Asn Ser Ser Ser Arg Ala Gln Leu Ser Asp Ala Leu Pro Glu Ser Glu
 65 70 75 80

Lys Ser Gln Ser Ala Gly Gln Val Ile Val Pro Thr Arg Met Gln Glu
 85 90 95

Leu Leu Asp Arg Gly Arg Pro Ile Glu Ala Ala Gln Phe Phe Leu Glu
 100 105 110

Thr His Ala Ala Ser Leu Lys Gly Ile Ser Ser Asp Arg Lys Glu Met
 115 120 125

Ala Thr Lys Val Phe Phe Val Asn Cys Lys Glu Asp Asn Val Phe Ile
 130 135 140

Ala Arg Ser Val Phe Glu Arg Leu Glu Glu Val Asp Arg Ile Thr Pro
 145 150 155 160

Glu Met Trp Lys Thr Leu Met Leu Ala Leu Ala Lys Lys Gly Cys Ile
 165 170 175

Glu Ser Val Ala Ser Val Tyr Thr Arg Tyr Met Arg Lys Phe Pro Cys
 180 185 190

Pro Pro Glu Met Val Asp Val Val Leu Arg Ser Leu Leu Glu Ser His
 195 200 205

Arg Leu Thr Thr Ala Lys Trp Phe Leu Leu Arg Asn Leu Gln His Asp
 210 215 220

Arg Asp Cys Gly Leu Cys Gly Ala Tyr Leu Ser Gly Leu Trp Arg Lys
 225 230 235 240

Thr Arg Ser Ile Glu Leu Leu Asn Gly Gln Leu Lys Lys Ile Leu Thr
 245 250 255

Ile Leu Pro Lys Phe Glu Lys Gln Pro Ser Asp Lys Leu Phe Asn Pro
 260 265 270

Val Ile Lys Ala Tyr Val Glu Phe Gly Arg Val Ala Asp Ala Glu Ala

275					280					285					
Leu	Val	His	Asp	Met	Thr	Thr	Leu	Tyr	Gly	Ile	Pro	Leu	Arg	Cys	Arg
290						295					300				
Thr	Gln	Gly	Leu	Leu	Val	Tyr	Ala	Lys	Ala	Leu	Asn	Cys	Asp	Trp	Glu
305					310					315					320
Gly	Val	Asp	Ala	Gly	Leu	Gln	Glu	Met	His	Lys	Leu	Lys	Leu	Thr	Arg
				325					330					335	
Arg	Arg	Arg	Asp	Phe	Leu	Pro	Ile	Phe	Asp	Arg	Ile	Phe	Leu	Glu	Tyr
			340					345					350		
Trp	Val	Ser	His	Ser	Gly	Ile	Glu	Ile	Arg	Asn	Phe	Val	Phe	Arg	Tyr
	355						360					365			
Leu	Asp	Lys	Phe	Asp	Ile	Val	Pro	Asp	Arg	Val	Leu	Tyr	Lys	His	Ile
370						375				380					
Leu	Glu	Ala	Phe	Val	Glu	Lys	Gly	Asp	Lys	Glu	Met	Ile	Ala	Glu	Phe
385					390					395					400
Thr	Ser	Met	Ala	Lys	Gln	Arg	Ser	Trp	Asn	Ile	Pro	Ile	Asn	Glu	Gln
				405					410					415	
Gln	Phe	Leu	Glu	Ile	Leu	Arg	Ser	Arg	Arg	Leu	Ala	Leu	Glu	Gly	Ala
			420					425					430		
Pro	Val	Gly	Phe	Trp	Gln	Met	Leu	Gln	Ala	Ala	Arg	Val	Lys	Tyr	Gly
	435					440						445			
His	Ser	Ser	Thr	Ser	Gln	Arg	Ile	Met	Gly	Tyr	Asp	Gln	Gln	Ser	Phe
	450					455					460				
Pro	Leu	Pro	Glu	Val	Asn	Ser	Met	Pro	Tyr	Thr	Gln	Asn	Pro	Leu	Ser
465					470					475					480
Trp	Tyr	Gln	Arg	Thr	Met	Gln	Glu	Thr	Thr	Pro	Ser	Lys	Pro	Val	Asp
				485					490					495	
Gln	Tyr	Gln	Lys	Leu	His	Lys	Gln	Met	Thr	His	Phe	Leu	His	Ala	Gly
			500					505					510		
Lys	Leu	Lys	Glu	Ala	Leu	Lys	Cys	Phe	Gln	Asn	Ala	Lys	Asn	Ala	Arg
	515						520					525			
Phe	Gln	Met	Arg	Gln	Leu	His	Val	Glu	Leu	Ala	Val	Ile	Ala	Thr	Leu
	530					535					540				
Leu	Glu	Asp	Gly	Leu	Ser	Ala	Ala	Arg	Ser	Leu	Ile	Glu	Ser	Glu	Trp
545					550					555					560
Arg	Thr	Ile	Arg	His	Leu	Val	Arg	Phe	Ser	Pro	Ile	Phe	Phe	Arg	Gln
				565					570					575	
Val	Met	Ala	Val	Asp	Glu	Asp	Ala	Gly	Gly	His	Ile	Val	Gln	Met	Ala
			580					585					590		
Val	Leu	Arg	Phe	Tyr	Gln	Leu	Cys	Trp	Ser	Thr	Lys	His	Met	Lys	Val
	595						600					605			

Lys His His Leu Thr Val Ala Thr Ser Arg Arg Leu Ile Ser Gln His
 610 615 620
 Lys Pro Glu Met Ala Leu Glu Leu Leu Thr Ala Val Tyr Lys Ser Arg
 625 630 635 640
 Tyr Arg Phe Ala Ala Thr Phe Asp Gly Val Cys Met Lys Met Phe Ala
 645 650 655
 Arg Ala Phe Ala Ala Thr Asp Asn Ile Leu Gly Leu Arg Trp Cys Ile
 660 665 670
 Leu Thr Ala Leu Ser Arg Asp Ser Ala Leu Asn His Asp Phe Val Val
 675 680 685
 Glu Val Arg Arg Ile Leu Gly Thr Leu Ser Pro Pro Ser Ala Val Asp
 690 695 700
 Ala Thr Ala Gly Pro Val Thr His Glu Gln Leu Glu Tyr Leu Tyr Tyr
 705 710 715 720
 Ile Ala Asp Leu Leu Glu Glu Lys Asn Glu Gly Cys Ala Pro Ile Trp
 725 730 735
 Glu Leu Lys His Asp Ala Thr Leu Lys Gln Ser Ser Arg Arg Gln Leu
 740 745 750
 Lys Gln Pro Leu Asp Ala Ser Arg Leu Phe Asn Gln Ser Asp Val Arg
 755 760 765
 Glu Thr Val Lys Arg Trp Asp Glu Glu Tyr Glu Leu Glu Ala Val Leu
 770 775 780
 Gly
 785

<210> 61
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer Impl

<400> 61
 atgaagcggt aagttccttg c

21

<210> 62
 <211> 19
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer Imp2

<400> 62
 gtgtggagga agaaagagc

19

<210> 63
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer ppyr1

<400> 63
ggaagacggg cagttagtcc

20

<210> 64
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer ppyr3

<400> 64
cccaggcttt acactttatg c

21

<210> 65
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer PCRa1 1

<220>
<223> misc_feature
<223> (21)..(30)
<223> n is a, c, g, or t

<400> 65
ggccacgcgt cgactagtag nnnnnnnnnn gatat

35

<210> 66
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer PCRa1 3

<220>
<223> misc_feature
<223> (21)..(30)
<223> n is a, c, g, or t

<400> 66
ggccacgcgt cgactagtac nnnnnnnnnn acgtc

35

<210> 67
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer PCRa1 4

<220>
<223> misc_feature
<223> (21)..(30)
<223> n is a, c, g, or t

<400> 67
ggccacgcgt cgactagtac nnnnnnnnnn tggac

35

<210> 68
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer PCRa1 5

<220>
<223> misc_feature
<223> (21)..(30)
<223> n is a, c, g, or t

<400> 68
ggccacgcgt cgactagtac nnnnnnnnnn acgtg

35

<210> 69
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer ppyr2N

<400> 69
cgaagttgac gttcagtatg c

21

<210> 70
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer ppyr4N

<400> 70
tgaccatgat tacgccaagc

20

<210> 71
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer PCRa1 2N

<400> 71
ggccacgcgt cgactagtac 20

<210> 72
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer 10.175.2

<400> 72
gttgatcctt tgggttctg 19

<210> 73
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer 10.304.4

<400> 73
cgcgatctg atgacatagc 20

<210> 74
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer 10.4.20.2

<400> 74
ctcttcgctt catcgtagcc 20

<210> 75
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer 11.4.9.4

<400> 75
attagtccat gcgagcatcc 20

<210> 76

<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer 11.6.20.2

<400> 76
gcctgagcct agtccatcac 20

<210> 77
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer 2.1.1.1

<400> 77
ctcgcaggtc gatttcactc 20

<210> 78
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer 2.1.1.2

<400> 78
ggaggaaacc ttgtcaccac 20

<210> 79
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer 2.1.1.5

<400> 79
taccgagaag gaggtcatgg 20

<210> 80
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer 2.1.1.6

<400> 80
tccagtcaag gttggtgatg 20

<210> 81
<211> 19

<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer 2.1.1.9

<400> 81
cgagaccatc ctacctcag

19

<210> 82
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer 4.3.4.2

<400> 82
acactcaccg ccttaaccac

20

<210> 83
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer 5.3.11.2

<400> 83
agtgcccttc attcagttcc

20

<210> 84
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer 6.8.13.2

<400> 84
gcgactttga gggaactatc c

21

<210> 85
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer 7.5.9.3

<400> 85
caccaccac cttatgaagc

20

<210> 86
<211> 20
<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer 7.5.9.4

<400> 86

accaggagaa tcagcgacac

20

<210> 87

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer 8.62.2

<400> 87

gggacgaaga atacgagctg

20

<210> 88

<211> 19

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer Gt11f1

<400> 88

ctgaatatcg acggtttcc

19

<210> 89

<211> 19

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer Gt11f3

<400> 89

gcacattggc tgaatatcg

19

<210> 90

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer Gt11Rev

<400> 90

ttgacaccag accaactggt aatg

24

<210> 91

<211> 3052

<212> DNA

<213> Aspergillus fumigatus

<220>

<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 91

```

cgagccgctc caagctattc gggatgagac tccggacgcg atccaggaga acacgattgg      60
attagaacaa ttgaaggagg ccatgtccaa agaacgagtc gtaggacgga gcagaaggat      120
acatcgcgct gagagcgcca gaaatgaccg cccggacgga gatgcttggg atgggaatgc      180
gcttggctat gcgtccagga ctaaggggaa gttctttgtc gttgagacag gcaatgaacc      240
tggcaattga ttcggcatgc ctctttccca aaagccattt caatattact gcacaatagc      300
ctgcttcate ttgctgcgca cgggctgcac ccctgctatg agagaccgcg cgatcctgct      360
gtgctgagtc agcattggat tacttcatta gacctcgaca gtcaacagca tttctccact      420
taaccaccta caacctaaaga cagcacggga actggttata tttgttcgag tcagtacttt      480
caggggtgtt tattaaatca atgtggaagt cttttaaaga aaagcatgcc agcaagtttg      540
ggggaggctc ggctgaagcg gcagcctcag acggtggcca agatctgacc acgatattgg      600
atagatccca acgcggggaa ttgacagtgc ttgttgcgct aatcgcacag cggatgcggg      660
atggaataga acaaaacttc tccaatgctc ctcttcgctc aggccagtct gtcaactacg      720
aagaaaaacg gacaggctcc ctgccccaat ctacagatgc acaagaagac cagtcatcct      780
ccggcagcgc agcgaacggt tcaagaaccc accctcaatt caaagacccg gagactgcga      840
catgtgcact atctaaatat gatgactgga gggactccgt ccttcttcga attggtgaag      900
tcgtcaacag ggaaccagaa catggtgaag ttcaggcgaa tgaaaaccca ccctcaggac      960
agcaatccca gcagatccgc tccgaggagg atgaccgttc cattcgtaag ctacgtgagg      1020
tctttccgcc ggtggagacc agcctctctc aattgccaga agcgaagaaa ctcttaattc      1080
tccactcatt gctactccta gttttgagtc ttgaacacta taacgcctgg tctcgggtcc      1140
tgatgctgtt cgtgacgtcc agcttagggc tggacgtgaa attactaaac gaagatgaag      1200
tcaaagtggc gaggggggtt cttgacactg ctctggcact gtcgtctaac gccccaggc      1260
aggatgagag tcgaagtcgc gattcatccc gaaaatggaa ggttgggata gcgtcagttg      1320
cgggtgctgc cctgatcggg atcactgggt gactggctgc gcccttgtt gcagctgggc      1380
ttggtactgt catgggcggc cttgggcttg gcgcaccgc cgcagcaggg tatctcggag      1440
ctctcgctgg aagtgggtt gtcgtcggcg gacttttcgg tgcttatggt gggcggatga      1500
ccggtcgtat ggttgacaag tacgcacggg aggtggatga ttttgccctt ctgccgatc      1560
gtggttctcg gcatcgatcc gaagacgaaa gagaagctgc ccatcaggat caccggctgc      1620
gggttaccat cggcgtgacc ggatggctga cagaggagga caatttcgtg atcccgtggc      1680
gagtgatcgg agcggaatcg gagtggttg gtctccgctg ggaaaccgag cccctgatga      1740
atctgggaaa tgcgcttgac cttttggtta ccagcgcgc atggactgcc ggtgaacaag      1800
tcctgaagaa gacattcctc tcccaactct tgaccgtagc gaaggctcgg gcggacaagg      1860
tcaaggtcgc acgtgtggtg gacaatccgt ttaccgtagc gaaggctcgg gcggacaagg      1920
ctggggaggt tctcgcggat gctcttatca gtaaagtgc gggcgagcga ccagtcaccc      1980
tcattggcta ctcttaggg tctcgggtga ttttcgcttg cttcaaagc ttggcgaaac      2040
ggcgcgcgtt cggcttggtg gaatccgcaa ttctgatgg agctcccacc ccgtcgaatt      2100
cagaacaatg gtgtcgcata cgcagtgttg tgagtggacg ccttgtaaac gtgtactcgg      2160
aaaacgactc cgtgctggct ctcttatatc gaacaagcag cctccagctt ggggttgacg      2220
gcttgacagc tggtgaagggt gtctcaggcg ttgagaatct ggacgttagc gacctgatca      2280
gcggccatct ccgttatcag tttctcgttg gcaggatctt gagcgttggt ggacttgaga      2340
gcattgatgc tcgcgaggtc gcactggagg aggcgcatt agaagccaaa gatcggaggc      2400
aggagcagga aagggtcat aacgaacgac aggtggatt tatgggcgag ggtcggtcac      2460
caagccagcg gctggaaagc caggaggatc tgcaggcgca agaggacaga ttacagaaag      2520
agatgggaaa agcacgagtg cggcactctt agatagtaca tttcaaagcg aatggaacaa      2580
tagctatgat gatttttctt tttctttctg gttatattag agatggacgt ctaaaatcat      2640
tatcccacaa tgatcgaagc agtggaaatg atacatgagg gacacgcaat caggtcagtc      2700
agcagtcgca gtctacccaa ggtaaaactca cggacagcag ctaatatccg acagatccgg      2760
gacaattcat ctgaatttga ggctaaaata tgaccaacca agcctccaac caaccccgcc      2820
agtcactggg gctgcaaagc ttggtctagt gaaagttagc gatcactagt ccaggcaacc      2880
gtgcatcaaa tggcctgtat gcgaacatgg tccctgggta acggaagcca gtctgtttcc      2940
aagcgaggtc aatttcaacg gtgtcctctc tagtggttgt ctctctgcaa ccaggcatgg      3000
tatgatttgt cggcctttag tgccatttcc tgagtcaagc aggacaggtc aa      3052

```

<210> 92

<211> 2052

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
Genomic sequence containing the coding region

<400> 92

atgtggaagt	cttttaaaga	aaagcatgcc	agcaagtttg	ggggaggctc	ggctgaagcg	60
gcagcctcag	acggtggcca	agatctgacc	acgatattgg	atagatccca	acgcggggaa	120
ttgacagtgc	ttgttgcgct	aatcgcacag	cggatgcggg	atggaataga	acaaaacttc	180
tccaatgctc	ctccttcgct	aggccagtct	gtcaactacg	aagaaaaacg	gacaggctcc	240
ctgccccaat	ctacagatgc	acaagaagac	cagtcatcct	ccggcagcgc	agcgaacggt	300
tcaagaaccg	accctcaatt	caaagaccgc	gagactgcga	catgtgcact	atctaaatat	360
gatgactgga	gggactccgt	ccttcttcga	attggtgaag	tcgtcaacag	ggatccagaa	420
catggtgaag	ttcaggcgaa	tgaaaaccca	ccctcaggac	agcaatccca	gcagatccgc	480
tccgaggagg	atgaccgttc	cattcgtaag	ctacgtgagg	tctttccgcc	ggtggagacc	540
agcctctctc	aattgccaga	agcgaagaaa	ctcttaattc	tccactcatt	gctactccta	600
gttttgagtc	ttgaacacta	taacgcctgg	tctcgggtcc	tgatgctgtt	cgtgacgtcc	660
agcttagggc	tgagcgtgaa	attactaaac	gaagatgaag	tcaaagtggc	gaggggggtg	720
cttgacactg	ctctggcact	gtcgtctaac	gccccaaagg	aggatgagag	tcgaagtgcg	780
gattcatccc	gaaaatggaa	ggttgggata	gcgtcagttg	cgggtgctgc	cctgatcggg	840
atcactggtg	gactggctgc	gccccttggt	gcagctgggc	ttggtactgt	catgggcggc	900
cttgggcttg	gcgccaccgc	cgcagcaggg	tatctcggag	ctctcgtcgt	aagtgggtgt	960
gtcgtcggcg	gacttttcgg	tgcttatggg	gggcggatga	ccggtcgtat	ggttgacaag	1020
tacgcacggg	aggtggatga	ttttgccttt	ctgccgattc	gtggttctcg	gcacgcgatc	1080
gaagacgaaa	gagaagctgc	ccatcaggat	caccggctgc	gggttaccat	cggcgtgacc	1140
ggatggctga	agaggaggga	caatttcgtg	atcccgtggc	gagtgatcgg	agcggaatcg	1200
gaggtgtttg	gtctccgctg	ggaaaccgag	cccctgatga	atctgggaaa	tgcgcttgac	1260
cttttggtaa	ccagcgccgc	atggactgcc	ggtgaacaag	tcctgaagaa	gacattcctc	1320
tcccaactct	tgaccgctgt	cgcgctgccg	cttggccttc	tcaaggctcg	acgtgtggtg	1380
gacaatccgt	ttagcgtagc	gaaggctcgg	gcggacaagg	ctggggagggt	tctcgcggat	1440
gctcttatca	gtaaagtgca	gggcgagcga	ccagtcaccc	tcattggcta	ctccttaggg	1500
tctcgggtga	ttttcgcttg	ccttcaaaag	ttggcgaaac	ggcgcgcggt	cggcttggtg	1560
gaatccgcaa	ttctgatggg	agctcccacc	ccgtcgaatt	cagaacaatg	gtgtcgcgac	1620
cgcagtgttg	tgagtggacg	ccttgtcaac	gtgtactcgg	aaaacgactc	cgtgctggct	1680
ctcttatata	gaacaagcag	cctccagctt	ggggttgacg	gcttgacagg	tggtgaaggt	1740
gtctcaggcg	ttgagaatct	ggacgttagc	gacctgatca	gcggccatct	ccgttatcag	1800
tttctcggtg	gcaggatctt	gagcgttggt	ggacttgaga	gcattgatgc	tcgcgaggtc	1860
gcactggagg	aggccgcatt	agaagccaaa	gatcggaggc	aggagcagga	aagggtcat	1920
aacgaacgac	aggctggatt	tatgggcgag	ggtcggtcac	caagccagcg	gctggaaagc	1980
caggaggatc	tgcagggcga	agaggacaga	ttacagaaaag	agatgggaaa	agcacgagtg	2040
cggcactctt	ag					2052

<210> 93

<211> 2052

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
Coding region without introns

<400> 93

atgtggaagt	cttttaaaga	aaagcatgcc	agcaagtttg	ggggaggctc	ggctgaagcg	60
gcagcctcag	acggtggcca	agatctgacc	acgatattgg	atagatccca	acgcggggaa	120
ttgacagtgc	ttgttgcgct	aatcgcacag	cggatgcggg	atggaataga	acaaaacttc	180
tccaatgctc	ctccttcgct	aggccagtct	gtcaactacg	aagaaaaacg	gacaggctcc	240
ctgccccaat	ctacagatgc	acaagaagac	cagtcatcct	ccggcagcgc	agcgaacggt	300
tcaagaaccg	accctcaatt	caaagaccgc	gagactgcga	catgtgcact	atctaaatat	360

```

gatgactgga gggactccgt ccttcttcga attggtgaag tcgtcaacag ggatccagaa 420
catggtgaag ttcaggcgaa tgaaaaccca ccctcaggac agcaatccca gcagatccgc 480
tccgaggagg atgaccgttc cattcgtaag ctacgtgagg tctttccgcc ggtggagacc 540
agcctctctc aattgccaga agcgaagaaa ctcttaattc tccactcatt gctactccta 600
gttttgagtc ttgaacacta taacgcctgg tctcggtcc tgatgctgtt cgtgacgtcc 660
agcttagggc tggacgtgaa attactaaac gaagatgaag tcaaagtggc gagggggttg 720
cttgacactg ctctggcact gtcgtctaac gcccgaaggc aggatgagag tcgaagtcgc 780
gattcatccc gaaaatggaa ggttgggata gcgtcagttg cgggtgctgc cctgatcggg 840
atcactggtg gactggctgc gccccttggt gcagctgggc ttggtactgt catgggcggc 900
cttgggcttg gcgccaccgc cgcagcaggg tatctcggag ctctcgtggt aagtgggtgt 960
gtcgtcggcg gacttttcgg tgcttatggt gggcggatga ccggtcgtat ggttgacaag 1020
tacgcacggg aggtggatga ttttgccttt ctgccgattc gtggttctcg gcatcgatcc 1080
gaagacgaaa gagaagctgc ccatcaggat caccggctgc gggttacat cggcgtgacc 1140
ggatggctga cagaggagga caatttcgtg atcccgtggc gagtgatcgg agcggaatcg 1200
gaggtgtttg gtctccgctg ggaaaccgag cccctgatga atctgggaaa tgcgcttgac 1260
cttttggtaa ccagcgccgc atggactgcc ggtgaacaag tcctgaagaa gacattcctc 1320
tcccaactct tgaccgctgt cgcgctgccg cttggccttc tcaaggtcgc acgtgtggtg 1380
gacaatccgt ttagcgtagc gaaggctcgg gcggacaagg ctggggaggt tctcgcggat 1440
gctcttatca gtaaagtgca gggcgagcga ccagtcaccc tcattggcta ctcttaggg 1500
tctcgggtga ttttcgcttg ccttcaaagc ttggcgaaac ggcgcgctt cggcttggtg 1560
gaatccgcaa ttctgatggg agctcccacc ccgtcgaatt cagaacaatg gtgtcgcac 1620
cgcagtgttg tgagtggacg ccttgtcaac gtgtactcgg aaaacgactc cgtgctggct 1680
ctcttatatc gaacaagcag cctccagctt ggggttgacg gcttgacgcc tgttgaaggt 1740
gtctcaggcg ttgagaatct ggacgttagc gacctgatca gcggccatct ccgttatcag 1800
tttctcgttg gcaggatctt gagcgttgtt ggacttgaga gcattgatgc tcgcgaggtc 1860
gcactggagg aggccgcatt agaagccaaa gatcggaggc aggagcagga aagggtcat 1920
aacgaacgac aggctggatt tatgggcgag ggtcggtcac caagccagcg gctggaaagc 1980
caggaggatc tgcagggcga agaggacaga ttacagaaa agatgggaaa agcacgagtg 2040
cggcactctt ag 2052

```

<210> 94

<211> 683

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
Protein sequence

<400> 94

```

Met Trp Lys Ser Phe Lys Glu Lys His Ala Ser Lys Phe Gly Gly Gly
1           5           10           15

```

```

Ser Ala Glu Ala Ala Ala Ser Asp Gly Gly Gln Asp Leu Thr Thr Ile
          20           25           30

```

```

Leu Asp Arg Ser Gln Arg Gly Glu Leu Thr Val Leu Val Ala Leu Ile
35           40           45

```

```

Ala Gln Arg Met Arg Asp Gly Ile Glu Gln Asn Phe Ser Asn Ala Pro
50           55           60

```

```

Pro Ser Ser Gly Gln Ser Val Asn Tyr Glu Glu Lys Arg Thr Gly Ser
65           70           75           80

```

```

Leu Pro Gln Ser Thr Asp Ala Gln Glu Asp Gln Ser Ser Ser Gly Ser
85           90           95

```

```

Ala Ala Asn Gly Ser Arg Thr Asp Pro Gln Phe Lys Asp Pro Glu Thr

```

100						105						110					
Ala	Thr	Cys	Ala	Leu	Ser	Lys	Tyr	Asp	Asp	Trp	Arg	Asp	Ser	Val	Leu		
		115					120					125					
Leu	Arg	Ile	Gly	Glu	Val	Val	Asn	Arg	Asp	Pro	Glu	His	Gly	Glu	Val		
		130				135					140						
Gln	Ala	Asn	Glu	Asn	Pro	Pro	Ser	Gly	Gln	Gln	Ser	Gln	Gln	Ile	Arg		
145					150					155					160		
Ser	Glu	Glu	Asp	Asp	Arg	Ser	Ile	Arg	Lys	Leu	Arg	Glu	Val	Phe	Pro		
				165					170					175			
Pro	Val	Glu	Thr	Ser	Leu	Ser	Gln	Leu	Pro	Glu	Ala	Lys	Lys	Leu	Leu		
			180					185					190				
Ile	Leu	His	Ser	Leu	Leu	Leu	Leu	Val	Leu	Ser	Leu	Glu	His	Tyr	Asn		
		195					200					205					
Ala	Trp	Ser	Arg	Val	Leu	Met	Leu	Phe	Val	Thr	Ser	Ser	Leu	Gly	Leu		
		210				215					220						
Asp	Val	Lys	Leu	Leu	Asn	Glu	Asp	Glu	Val	Lys	Val	Ala	Arg	Gly	Leu		
225					230					235					240		
Leu	Asp	Thr	Ala	Leu	Ala	Leu	Ser	Ser	Asn	Ala	Pro	Arg	Gln	Asp	Glu		
				245					250					255			
Ser	Arg	Ser	Arg	Asp	Ser	Ser	Arg	Lys	Trp	Lys	Val	Gly	Ile	Ala	Ser		
			260					265					270				
Val	Ala	Gly	Ala	Ala	Leu	Ile	Gly	Ile	Thr	Gly	Gly	Leu	Ala	Ala	Pro		
		275					280					285					
Leu	Val	Ala	Ala	Gly	Leu	Gly	Thr	Val	Met	Gly	Gly	Leu	Gly	Leu	Gly		
		290				295					300						
Ala	Thr	Ala	Ala	Ala	Gly	Tyr	Leu	Gly	Ala	Leu	Ala	Gly	Ser	Gly	Val		
305					310					315					320		
Val	Val	Gly	Gly	Leu	Phe	Gly	Ala	Tyr	Gly	Gly	Arg	Met	Thr	Gly	Arg		
				325					330					335			
Met	Val	Asp	Lys	Tyr	Ala	Arg	Glu	Val	Asp	Asp	Phe	Ala	Phe	Leu	Pro		
			340					345					350				
Ile	Arg	Gly	Ser	Arg	His	Arg	Ser	Glu	Asp	Glu	Arg	Glu	Ala	Ala	His		
		355					360					365					
Gln	Asp	His	Arg	Leu	Arg	Val	Thr	Ile	Gly	Val	Thr	Gly	Trp	Leu	Thr		
		370				375					380						
Glu	Glu	Asp	Asn	Phe	Val	Ile	Pro	Trp	Arg	Val	Ile	Gly	Ala	Glu	Ser		
385					390					395					400		
Glu	Val	Phe	Gly	Leu	Arg	Trp	Glu	Thr	Glu	Pro	Leu	Met	Asn	Leu	Gly		
				405					410					415			
Asn	Ala	Leu	Asp	Leu	Leu	Val	Thr	Ser	Ala	Ala	Trp	Thr	Ala	Gly	Glu		
			420					425					430				

Gln Val Leu Lys Lys Thr Phe Leu Ser Gln Leu Leu Thr Ala Val Ala
 435 440 445
 Leu Pro Leu Gly Leu Leu Lys Val Ala Arg Val Val Asp Asn Pro Phe
 450 455 460
 Ser Val Ala Lys Ala Arg Ala Asp Lys Ala Gly Glu Val Leu Ala Asp
 465 470 475 480
 Ala Leu Ile Ser Lys Val Gln Gly Glu Arg Pro Val Thr Leu Ile Gly
 485 490 495
 Tyr Ser Leu Gly Ser Arg Val Ile Phe Ala Cys Leu Gln Ser Leu Ala
 500 505 510
 Lys Arg Arg Ala Phe Gly Leu Val Glu Ser Ala Ile Leu Met Gly Ala
 515 520 525
 Pro Thr Pro Ser Asn Ser Glu Gln Trp Cys Arg Ile Arg Ser Val Val
 530 535 540
 Ser Gly Arg Leu Val Asn Val Tyr Ser Glu Asn Asp Ser Val Leu Ala
 545 550 555 560
 Leu Leu Tyr Arg Thr Ser Ser Leu Gln Leu Gly Val Ala Gly Leu Gln
 565 570 575
 Pro Val Glu Gly Val Ser Gly Val Glu Asn Leu Asp Val Ser Asp Leu
 580 585 590
 Ile Ser Gly His Leu Arg Tyr Gln Phe Leu Val Gly Arg Ile Leu Ser
 595 600 605
 Val Val Gly Leu Glu Ser Ile Asp Ala Arg Glu Val Ala Leu Glu Glu
 610 615 620
 Ala Ala Leu Glu Ala Lys Asp Arg Arg Gln Glu Gln Glu Arg Ala His
 625 630 635 640
 Asn Glu Arg Gln Ala Gly Phe Met Gly Glu Gly Arg Ser Pro Ser Gln
 645 650 655
 Arg Leu Glu Ser Gln Glu Asp Leu Gln Gly Glu Glu Asp Arg Leu Gln
 660 665 670
 Lys Glu Met Gly Lys Ala Arg Val Arg His Ser
 675 680

<210> 95

<211> 3814

<212> DNA

<213> *Aspergillus fumigatus*

<220>

 <223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 95

ctttagtagc agttgtttct gaattattgca gtcatttcaa agagtccacg atgaagctca

60

gaggagctgc	ttacgattat	atcgctaaaa	gtacattaag	ggacgctctt	tgaaactttg	120
tgttgacgt	cacttatata	gatcgaaggg	tttgcaggaa	aataggagac	tactccatgt	180
aggtaggtag	cattttacta	tcgacgtgga	tagttgtcgt	atgatctgag	ctggatccgg	240
agagcgatcg	gaggactacg	gcacgtgaca	aagcctgcga	gtgcaccgcc	atgcaaactt	300
tccgctggag	ctcagcaaaa	agtccaccga	aattgccctg	ttgaatattc	caaccaattt	360
gtgcccattg	tcgtccccc	acttttcttt	cgggcattgt	ccccattagt	tgagctttat	420
ctcagtttac	tgtttatata	aatgcttcgc	aggtgacgcc	catagaacct	gccgcctgcg	480
gtgcaagagg	ttctaccacc	atgttctcga	aaccaacca	cagccccccg	gctgtccctt	540
ctcgaaatgc	tctccgagtt	ctgcgtagat	tagcgcttgc	cggctcaact	gtgggcagtt	600
tctgcacggg	cgcgcccatc	acctacgatg	tccatcgccg	agtccgagtc	gccgagcgca	660
ttgtcgagaa	caaacggggc	ttacagacct	cgcacccaa	ctacgatgcc	acgtctgccg	720
cgaacgact	cgcccgatag	atggaagcag	cggaaagcag	cgaatttatg	ggattggcgt	780
cgttgaagga	ggcggacaga	aagatccgag	aagggcaagc	tacgcaggat	gacgatgtgg	840
tagctttgca	ccaggagggg	ggctttcgac	gtccgggcat	ggggttgagg	gatccgcggc	900
gagcagtcca	ggcagagtcg	tatctggaga	ctaccgggtc	gcagctcgtc	gatgcgctta	960
tatcacggcc	gaatcttgag	agtggcttgg	gtcgaaggaa	ttttgttcct	cctaggcagg	1020
tcccggttgt	cgacgccatg	gagcggacga	aaaatgctat	acaatcaa	aattccagct	1080
cgcgggcgca	actttcggat	gcattaccgc	agagcgagaa	atcacagagt	gcagggcagg	1140
ttattgtccc	gacacggatg	caggaacttc	tcgacgcggg	tcgtcccatt	gaggcgggcc	1200
aattttttct	ggagacacat	gccgcttcat	tgaaggcat	atcctcagac	aggaaggaaa	1260
tggctacgaa	ggtattcttc	gtcaactgca	aagaggacaa	tgtgtttatt	gccagaagtg	1320
tgtttgagcg	ggttgaagag	gtggatagaa	tcacgcctga	gatgtggaag	acgttgatgc	1380
tggctttggc	gaagaaaggg	tgcattgaat	cagttgcgag	tgtttatacg	cgatacatgc	1440
gcaagttccc	ttgccctccg	gagatggctg	acgttgtgct	gcggagtttg	cttgaatccc	1500
accgactcac	cactgcgaaa	tggttcctct	tgcgcaatct	acaacatgac	cgtgattgcg	1560
gtttgtgcgg	agcctacctc	tccggcctgt	ggcgggaagac	aagaagcatc	gagttattga	1620
acgggcagtt	gaaaaagata	ttgaccattc	ttccaaagtt	cgaaaaacaa	cctagcgaca	1680
aactatttaa	cccggtgatc	aaggcatatg	ttgaatttgg	gcgggttgcc	gatgccgaag	1740
ctctggtgca	tgatatgacc	actttatatg	ggatccctct	tcgttgccga	actcaggggc	1800
tattggtata	cgccaaggct	ctgaaactgtg	actgggaggg	agttgacgca	ggactgcaag	1860
agatgcacaa	actcaagctg	acgagacgcc	ggcgagactt	ccttcctatt	tttgatcgaa	1920
tattttctgga	gtactgggtc	tcacattcgg	gaattgagat	tcgcaatttt	gtgttccggg	1980
accttgataa	attcgacatt	gtccccgatc	gcgtgctcta	caagcacatc	ttggaggcct	2040
tcgtggagaa	aggagacaag	gaaatgattg	ctgaattttac	aagtatggcg	aagcagcgat	2100
cgtggaatat	ccccataaac	gagcagcaat	tcttgagatg	actacgggtc	cgtcgccctg	2160
cattggaagg	agcaccagtg	gggttctggc	aaatgctgca	ggcagcgcg	gtcaagtacg	2220
ggcacagctc	cacgtctcag	cgtatcatgg	gctacgacca	acagtcattc	cctttgccgg	2280
aagtcaacag	catgccatat	acacagaatc	gcgtatcgtg	gtaccagaga	acgatgcaag	2340
agaccacgca	gtcgaaagct	gtcgaccaat	atcagaaact	ccataagcag	atgaccattt	2400
ttctgcacgc	tggaagagct	aaggaagcat	tgaagtgtct	tcaaaatgct	aaaaatgcc	2460
ggttccagat	gaggcagctt	cacgttgaat	tggcggtcat	agcgactttg	cttgaggacg	2520
gccttagtgc	agcgcgagtg	ctcatcgagt	ctgaatggcg	gactatccgt	caccttgctc	2580
gcttctctcc	tatcttcttt	cgtcaagtca	tggcggtcga	cgaggatgcg	ggtggccaca	2640
ttgtccagat	ggcagtccta	cgcttctacc	agctttgttg	gtctacgaaa	cacatgaagg	2700
tcaagcatca	ccttactgtt	gcgacaagcc	gtcgtttgat	ctcccaacat	aagccggaaa	2760
tggctctgga	gcttctgacg	gccgtgtaca	agtcocgtta	taggtttgca	gcgacctttg	2820
acggggtttg	catgaagatg	tttgcgcg	ccttcgcgcg	gacagacaac	attctaggct	2880
tacgatggtg	tattcttact	gctttatcac	gcgatagtgc	actcaatcat	gattttgtgg	2940
tggaaagtctg	ccgaatcttg	ggcactctaa	gtccaccttc	cgcggtggat	gccaccgccg	3000
gccccgtcac	tcatgagcag	ctggaatacc	tttattacat	cgccgatctg	ctcgaggaga	3060
agaatgaggg	gtgcgccccg	atatgggagc	tcaagcatga	cgccacactg	aagcagtcct	3120
cgaggcgaca	gttgaagcaa	cctcttgacg	caagccgtct	tttcaaccag	tccgatgtcc	3180
gcgagaccgt	caagcgatgg	gacgaagaat	acgagctgga	ggcagtgctg	ggtaggattg	3240
acaatgaccc	gaactcgatt	actgctcgat	ggaacgagag	tcgtcggtca	catcagaag	3300
aggcggtttt	atgacgatcg	gtctgatacc	atctaggaag	tgggtgcaac	tgcaacgcct	3360
ggccgagcct	ttattgaaatc	atgtgatagg	ctccttagcc	actgtatata	tactattgac	3420
actctgtact	ttactctcct	gtgcgggttg	tgactgccat	tattttctcat	cggaataga	3480
atagagatgg	tgagattgga	tgcaaataatc	acggatatgg	ccgaaacccc	ttggctctcc	3540
ttttgcaggc	aacaacgccg	aacggtatcc	aataataaac	actgtaattg	atcggatggg	3600
atcagaccag	aagatgctct	tttccggctc	tttcagtgat	catacggtgt	tcctgaattt	3660
tctctcacca	ataagaatct	agcactgcgg	aaggaggaaa	gccagtcctt	cacatgtcac	3720

gccactgtcc actcttggcc cctttccagt aaaaacactt aaagttctcc gatctttttc 3780
tatctccgcc atcccatcct tttcatcaat tgct 3814

<210> 96

<211> 2814

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466
Genomic sequence containing the coding region

<400> 96

atgttctcga	aaccaaccaa	cagccccccg	gctgtcccct	ctcgaaatgc	tctccgagtt	60
ctgcgtagat	tagcgcttgc	cggctcaact	gtgggcagtt	tctgcacggt	cgcgcccatc	120
acctacgatg	tccatcgccg	agtccgagtc	gccgagcgca	ttgtcgagaa	caaacggggc	180
ttacagacct	ccgcacccaa	ctacgatgcc	acgtctgccg	cgaaacgact	cgcccgtatg	240
atggaagcag	cggaagcagg	cgaatttatg	ggattggcgt	cgttgaagga	ggcggacaga	300
aagatccgag	aagggcaagc	tacgcaggat	gacgatgtgg	tagctttgca	ccaggagggg	360
ggctttcgac	gtccgggcat	gggggttgag	gatccgcggc	gagcagtcca	ggcagagtcg	420
tatctggaga	ctaccgggtc	gcagctcgtc	gatgcgctta	tatcacggcc	gaatcttgag	480
agtggcttgg	gtcgaaggaa	ttttgttcc	cctaggcagg	tcccggttgt	cgacgccatg	540
gagcggacga	aaaatgctat	acaatcaa	aattccagct	cgcgggcgca	actttcggat	600
gcattaccgc	agagcgagaa	atcacagagt	gcagggcagg	ttattgtccc	gacacggatg	660
caggaacttc	tcgaccgcgg	togtcccatt	gaggcggccc	aattttttct	ggagacacat	720
gccgcttcat	tgaaggcat	atcctcagac	aggaaggaaa	tggctacgaa	ggtattcttc	780
gtcaactgca	aagaggacaa	tgtgtttatt	gccagaagtg	tgtttgagcg	ggtggaagag	840
gtggatagaa	tcacgcctga	gatgtggaag	acgttgatgc	tggctttggc	gaagaaagg	900
tgcattgaat	cagttgcgag	tgtttatacg	cgatacatgc	gcaagttccc	ttgccctccg	960
gagatggtcg	acgtttgtct	gcgagagttg	cttgaatccc	accgactcac	cactgcgaaa	1020
tggttcctct	tgcgcaatct	acaacatgac	cgtgattgcg	gtttgtgcgg	agcctacctc	1080
tccggcctgt	ggcggaagac	aagaagcatc	gagttattga	acgggcagtt	gaaaaagata	1140
ttgaccattc	ttccaaagtt	cgaaaaacaa	cctagcgaca	aactatttaa	cccgggtgatc	1200
aaggcatatg	ttgaattttg	gcggggttgc	gatgccgaag	ctctggtgca	tgatatgacc	1260
actttatatg	ggatccctct	togttgccga	actcagggcc	tattggtata	cgccaaggct	1320
ctgaactgtg	actgggaggg	agttgacgca	ggactgcaag	agatgcacaa	actcaagctg	1380
acgagacgcg	ggcgagactt	ccttcctatt	tttgatcgaa	tatttctgga	gtactgggtc	1440
tcacattcgg	gaattgagat	tcgcaatttt	gtgttccgg	accttgataa	attcgacatt	1500
gtccccgatc	gcgtgctcta	caagcacatc	ttggaggctt	tcgtggagaa	aggagacaag	1560
gaaatgattg	ctgaattttac	aagtatggcg	aagcagcgat	cgtggaatat	ccccataaac	1620
gagcagcaat	tcttgagat	actacggtct	cgtcgccctg	cattggaagg	agcaccagtg	1680
gggttctggc	aaatgctgca	ggcagcgctg	gtcaagtacg	ggcacagctc	cacgtctcag	1740
cgtatcatgg	gctacgacca	acagtcattc	cctttgccgg	aagtcaacag	catgccatat	1800
acacagaatc	cgctatcgtg	gtaccagaga	acgatgcaag	agaccacgcc	gtcgaagcct	1860
gtcgaccaat	atcagaaact	ccataagcag	atgaccatt	ttctgcacgc	tggaaagctg	1920
aaggaagcat	tgaagtgctt	tcaaaatgct	aaaaatgcc	ggttccagat	gaggcagctt	1980
cacgttgaat	tggcggtcat	agcgactttg	cttgaggacg	gccttagtgc	agcgcgcagt	2040
ctcatcgagt	ctgaatggcg	gactatccgt	caccttgctc	gcttctctcc	tatcttcttt	2100
cgtcaagtca	tggcggtcga	cgaggatgcg	ggtggccaca	ttgtccagat	ggcagtccta	2160
cgcttctacc	agctttgttg	gtctacgaaa	cacatgaagg	tcaagcatca	ccttactgtt	2220
gogacaagcc	gtcgcttgat	ctcccaacat	aagccgaaaa	tggctctgga	gcttctgacg	2280
gccgtgtaca	agtcccgtta	taggttttga	gcgacctttg	acgggggttg	catgaagatg	2340
tttgcgcgcg	ccttcgccgc	gacagacaac	attctaggct	tacgatgggt	tattcttact	2400
gctttatcac	gcgatagtgc	actcaatcat	gattttgtgg	tggaaagtgc	ccgaatcttg	2460
ggcactctaa	gtccaccttc	cgcggtggat	gccaccgcgc	gccccgtcac	tcatgagcag	2520
ctggaatacc	tttattacat	cgccgatctg	ctcgaggaga	agaatgaggg	gtgcgccccg	2580
atatgggagc	tcaagcatga	cgccacactg	aagcagttct	cgaggcgaca	ggtgaagcaa	2640
cctcttgacg	caagccgtct	tttcaaccag	tccgatgtcc	gcgagaccgt	caagcgatgg	2700
gacgaagaat	acgagctgga	ggcagtgctg	ggtaggattg	acaatgaccc	gaactcgatt	2760
actgctcgat	ggaacgagag	tcgtcgttca	catcagaaag	aggcgggttt	atga	2814

<210> 97

<211> 2814

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466

Coding region without introns

<400> 97

atgttctcga	aaccaaccaa	cagccccccg	gctgtccctt	ctcgaaatgc	tctccgagtt	60
ctgcgtagat	tagcgcttgc	cggctcaact	gtgggcagtt	tctgcacggt	cgcggccatc	120
acctacgatg	tccatcgccg	agtccgagtc	gccgagcgca	ttgtcgagaa	caaacgggcc	180
ttacagacct	ccgcacccaa	ctacgatgcc	acgtctgccg	cgaaacgact	cgcccgtatg	240
atggaagcag	cggaagcagg	cgaatttatg	ggattggcgt	cgttgaagga	ggcggacaga	300
aagatccgag	aagggcaagc	tacgcaggat	gacgatgtgg	tagctttgca	ccaggagggg	360
ggctttcgac	gtccgggcat	ggggttgagg	gacccgcggc	gagcagtcca	ggcagagtcg	420
tatctggaga	ctaccgggtc	gcagctcgtc	gatgcgctta	tatcacggcc	gaatcttgag	480
agtggcttgg	gtcgaaggaa	ttttgttcc	cctaggcagg	tcccggttgt	cgacgccatg	540
gagcggagca	aaaatgctat	acaatcaa	aattccagct	cgcgggcgca	actttcggat	600
gcattaccgg	agagcgagaa	atcacagagt	gcagggcagg	ttattgtccc	gacacggatg	660
caggaaacttc	tcgaccgcgg	tcgtccatt	gaggcgggcc	aattttttct	ggagacacat	720
gccgcttcat	tgaaggcat	atcctcagac	aggaaggaaa	tggctacgaa	ggtattcttc	780
gtcaactgca	aagaggacaa	tgtgtttatt	gccagaagtg	tgtttgagcg	gttggaaagag	840
gtggatagaa	tcacgcctga	gatgtggaag	acgttgatgc	tggctttggc	gaagaaaagg	900
tgcattgaat	cagttgcbag	tgtttatacg	cgatacatgc	gcaagttccc	ttgccctccg	960
gagatggtcg	acgttgtgct	gcggaagttg	cttgaatccc	accgactcac	caactgcgaaa	1020
tggttcctct	tgcgcaatct	acaacatgac	cgtgattgcg	gtttgtgcgg	agcctacctc	1080
tccggcctgt	ggcggaagac	aagaagcatc	gagttattga	acgggcagtt	gaaaaagata	1140
ttgaccattc	ttccaaagtt	cgaaaaacaa	cctagcgaca	aactatttaa	cccggtgatc	1200
aaggcatatg	ttgaatttgg	gcggttgcc	gatgccgaag	ctctggtgca	tgatatgacc	1260
actttatatg	ggatccctct	tcgttgccga	actcagggcc	tattggtata	cgccaaggct	1320
ctgaactgtg	actgggaggg	agttgacgca	ggactgcaag	agatgcacaa	actcaagctg	1380
acgagacgcc	ggcgagactt	ccttcctatt	tttgatcgaa	tatttctgga	gtactgggtc	1440
tcacattcgg	gaattgagat	tcgcaatttt	gtgttccggt	accttgataa	attcgacatt	1500
gtccccgatc	gcgtgctcta	caagcacatc	ttggaggctt	tcgtggagaa	aggagacaa	1560
gaaatgattg	ctgaatttac	aagtatggcg	aagcagcgat	cgtggaatat	ccccataaac	1620
gagcagcaat	tcttgagat	actacggtct	cgctgcctcg	cattggaagg	agcaccagtg	1680
gggttctggc	aaatgctgca	ggcagcgctg	gtcaagtaag	ggcacagctc	cacgtctcag	1740
cgtatcatgg	gctacgacca	acagtcattc	cctttgccgg	aagtcaacag	catgccatat	1800
acacagaatc	cgctatcgtg	gtaccagaga	acgatgcaag	agaccacgcc	gtcgaagcct	1860
gtcgaccaat	atcagaaact	ccataagcag	atgacccatt	ttctgcacgc	tggaaagctg	1920
aaggaaagcat	tgaagtgtct	tcaaaatgct	aaaaatgcc	ggttccagat	gaggcagctt	1980
cacgttgaat	tggcggtcct	agcgactttg	cttgaggacg	gccttagtgc	agcgcgcagt	2040
ctcatcgagt	ctgaatggcg	gactatccgt	caccttgctc	gcttctctcc	tatcttcttt	2100
cgtcaagtca	tggcggtcga	cgaggatgcg	gggtggccaca	ttgtccagat	ggcagtccta	2160
cgcttctacc	agctttgttg	gtctacgaaa	cacatgaagg	tcaagcatca	ccttactgtt	2220
gcgacaagcc	gtcgcttgat	ctcccaacat	aagccggaaa	tggctctgga	gcttctgacg	2280
gccgtgtaca	agtcccgtaa	taggtttgca	gcgacctttg	acgggggttg	catgaagatg	2340
tttgcgcgcg	ccttcgccgc	gacagacaac	attctaggct	tacgatgggtg	tattcttact	2400
gctttatcac	gcgatagtgc	actcaatcat	gattttgtgg	tggaagttcg	ccgaatcttg	2460
ggcactctaa	gtccaccttc	cgcggtggat	gccaccgccg	gccccgtcac	tcatgagcag	2520
ctggaatacc	tttattacat	cgccgatctg	ctcgaggaga	agaatgaggg	gtgcgccccg	2580
atatggggagc	tcaagcatga	cgccacactg	aagcagtcct	cgaggcgaca	gttgaagcaa	2640
cctcttgacg	caagccgtct	tttcaaccag	tccgatgtcc	gcgagaccgt	caagcgatgg	2700
gacgaagaat	acgagctgga	ggcagtgctg	ggtaggattg	acaatgaccc	gaactcgatt	2760
actgctcgat	ggaacgagag	tcgtcgttca	catcagaaa	aggcgggttt	atga	2814

<210> 98
 <211> 937
 <212> PRT
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466
 Protein sequence

<400> 98

Met	Phe	Ser	Lys	Pro	Thr	Asn	Ser	Pro	Pro	Ala	Val	Pro	Ser	Arg	Asn	1	5	10	15
Ala	Leu	Arg	Val	Leu	Arg	Arg	Leu	Ala	Leu	Ala	Gly	Ser	Thr	Val	Gly	20	25	30	
Ser	Phe	Cys	Thr	Val	Ala	Ala	Ile	Thr	Tyr	Asp	Val	His	Arg	Arg	Val	35	40	45	
Arg	Val	Ala	Glu	Arg	Ile	Val	Glu	Asn	Lys	Arg	Ala	Leu	Gln	Thr	Ser	50	55	60	
Ala	Pro	Asn	Tyr	Asp	Ala	Thr	Ser	Ala	Ala	Lys	Arg	Leu	Ala	Arg	Met	65	70	75	80
Met	Glu	Ala	Ala	Glu	Ala	Gly	Glu	Phe	Met	Gly	Leu	Ala	Ser	Leu	Lys	85	90	95	
Glu	Ala	Asp	Arg	Lys	Ile	Arg	Glu	Gly	Gln	Ala	Thr	Gln	Asp	Asp	Asp	100	105	110	
Val	Val	Ala	Leu	His	Gln	Glu	Gly	Gly	Phe	Arg	Arg	Pro	Gly	Met	Gly	115	120	125	
Leu	Glu	Asp	Pro	Arg	Arg	Ala	Val	Gln	Ala	Glu	Ser	Tyr	Leu	Glu	Thr	130	135	140	
Thr	Arg	Ser	Gln	Leu	Val	Asp	Ala	Leu	Ile	Ser	Arg	Pro	Asn	Leu	Glu	145	150	155	160
Ser	Gly	Leu	Gly	Arg	Arg	Asn	Phe	Val	Pro	Pro	Arg	Gln	Val	Pro	Val	165	170	175	
Val	Asp	Ala	Met	Glu	Arg	Thr	Lys	Asn	Ala	Ile	Gln	Ser	Asn	Asn	Ser	180	185	190	
Ser	Ser	Arg	Ala	Gln	Leu	Ser	Asp	Ala	Leu	Pro	Glu	Ser	Glu	Lys	Ser	195	200	205	
Gln	Ser	Ala	Gly	Gln	Val	Ile	Val	Pro	Thr	Arg	Met	Gln	Glu	Leu	Leu	210	215	220	
Asp	Arg	Gly	Arg	Pro	Ile	Glu	Ala	Ala	Gln	Phe	Phe	Leu	Glu	Thr	His	225	230	235	240
Ala	Ala	Ser	Leu	Lys	Gly	Ile	Ser	Ser	Asp	Arg	Lys	Glu	Met	Ala	Thr	245	250	255	
Lys	Val	Phe	Phe	Val	Asn	Cys	Lys	Glu	Asp	Asn	Val	Phe	Ile	Ala	Arg	260	265	270	

Ser Val Phe Glu Arg Leu Glu Glu Val Asp Arg Ile Thr Pro Glu Met
 275 280 285
 Trp Lys Thr Leu Met Leu Ala Leu Ala Lys Lys Gly Cys Ile Glu Ser
 290 295 300
 Val Ala Ser Val Tyr Thr Arg Tyr Met Arg Lys Phe Pro Cys Pro Pro
 305 310 315 320
 Glu Met Val Asp Val Val Leu Arg Ser Leu Leu Glu Ser His Arg Leu
 325 330 335
 Thr Thr Ala Lys Trp Phe Leu Leu Arg Asn Leu Gln His Asp Arg Asp
 340 345 350
 Cys Gly Leu Cys Gly Ala Tyr Leu Ser Gly Leu Trp Arg Lys Thr Arg
 355 360 365
 Ser Ile Glu Leu Leu Asn Gly Gln Leu Lys Lys Ile Leu Thr Ile Leu
 370 375 380
 Pro Lys Phe Glu Lys Gln Pro Ser Asp Lys Leu Phe Asn Pro Val Ile
 385 390 395 400
 Lys Ala Tyr Val Glu Phe Gly Arg Val Ala Asp Ala Glu Ala Leu Val
 405 410 415
 His Asp Met Thr Thr Leu Tyr Gly Ile Pro Leu Arg Cys Arg Thr Gln
 420 425 430
 Gly Leu Leu Val Tyr Ala Lys Ala Leu Asn Cys Asp Trp Glu Gly Val
 435 440 445
 Asp Ala Gly Leu Gln Glu Met His Lys Leu Lys Leu Thr Arg Arg Arg
 450 455 460
 Arg Asp Phe Leu Pro Ile Phe Asp Arg Ile Phe Leu Glu Tyr Trp Val
 465 470 475 480
 Ser His Ser Gly Ile Glu Ile Arg Asn Phe Val Phe Arg Tyr Leu Asp
 485 490 495
 Lys Phe Asp Ile Val Pro Asp Arg Val Leu Tyr Lys His Ile Leu Glu
 500 505 510
 Ala Phe Val Glu Lys Gly Asp Lys Glu Met Ile Ala Glu Phe Thr Ser
 515 520 525
 Met Ala Lys Gln Arg Ser Trp Asn Ile Pro Ile Asn Glu Gln Gln Phe
 530 535 540
 Leu Glu Ile Leu Arg Ser Arg Arg Leu Ala Leu Glu Gly Ala Pro Val
 545 550 555 560
 Gly Phe Trp Gln Met Leu Gln Ala Ala Arg Val Lys Tyr Gly His Ser
 565 570 575
 Ser Thr Ser Gln Arg Ile Met Gly Tyr Asp Gln Gln Ser Phe Pro Leu
 580 585 590

Pro Glu Val Asn Ser Met Pro Tyr Thr Gln Asn Pro Leu Ser Trp Tyr
 595 600 605
 Gln Arg Thr Met Gln Glu Thr Thr Pro Ser Lys Pro Val Asp Gln Tyr
 610 615 620
 Gln Lys Leu His Lys Gln Met Thr His Phe Leu His Ala Gly Lys Leu
 625 630 635 640
 Lys Glu Ala Leu Lys Cys Phe Gln Asn Ala Lys Asn Ala Arg Phe Gln
 645 650 655
 Met Arg Gln Leu His Val Glu Leu Ala Val Ile Ala Thr Leu Leu Glu
 660 665 670
 Asp Gly Leu Ser Ala Ala Arg Ser Leu Ile Glu Ser Glu Trp Arg Thr
 675 680 685
 Ile Arg His Leu Val Arg Phe Ser Pro Ile Phe Phe Arg Gln Val Met
 690 695 700
 Ala Val Asp Glu Asp Ala Gly Gly His Ile Val Gln Met Ala Val Leu
 705 710 715 720
 Arg Phe Tyr Gln Leu Cys Trp Ser Thr Lys His Met Lys Val Lys His
 725 730 735
 His Leu Thr Val Ala Thr Ser Arg Arg Leu Ile Ser Gln His Lys Pro
 740 745 750
 Glu Met Ala Leu Glu Leu Leu Thr Ala Val Tyr Lys Ser Arg Tyr Arg
 755 760 765
 Phe Ala Ala Thr Phe Asp Gly Val Cys Met Lys Met Phe Ala Arg Ala
 770 775 780
 Phe Ala Ala Thr Asp Asn Ile Leu Gly Leu Arg Trp Cys Ile Leu Thr
 785 790 795 800
 Ala Leu Ser Arg Asp Ser Ala Leu Asn His Asp Phe Val Val Glu Val
 805 810 815
 Arg Arg Ile Leu Gly Thr Leu Ser Pro Pro Ser Ala Val Asp Ala Thr
 820 825 830
 Ala Gly Pro Val Thr His Glu Gln Leu Glu Tyr Leu Tyr Tyr Ile Ala
 835 840 845
 Asp Leu Leu Glu Glu Lys Asn Glu Gly Cys Ala Pro Ile Trp Glu Leu
 850 855 860
 Lys His Asp Ala Thr Leu Lys Gln Ser Ser Arg Arg Gln Leu Lys Gln
 865 870 875 880
 Pro Leu Asp Ala Ser Arg Leu Phe Asn Gln Ser Asp Val Arg Glu Thr
 885 890 895
 Val Lys Arg Trp Asp Glu Glu Tyr Glu Leu Glu Ala Val Leu Gly Arg
 900 905 910
 Ile Asp Asn Asp Pro Asn Ser Ile Thr Ala Arg Trp Asn Glu Ser Arg

915

920

925

Arg Ser His Gln Lys Glu Ala Gly Leu
930 935

<210> 99

<211> 2401

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 99

```

acatggatga atcactgccc gatatcgaga agtcgcttga accgtacctc tcacattttg      60
gttatcggag tgacggatcg gatcagagcg cagtatttga tcttttagaa agtgagcgtt      120
tcactcataa caagagcccc ttgacagaca ttcgcaaggg ttaacctcat ggttgtggtt      180
tggtttggtt tgctctgctt ataattctct cggcattgtcg gtaatcaatc cacttttctc      240
tggggccctt ctacacatgc agcaatttca ttggtcatct gagatataca gatttgtaag      300
gcagtatcag tatcatcagg atacgcttct atgtagtatg agctcaaaga acagatagtt      360
gagaagtagt actgatatac cgtggtttaa gtattttgtc ggagtgtctaa gcattacaag      420
tggcatatcc tttcagaata gaaaaccatc aggcaaagcg gattatcacc agaatttcca      480
tctcagtcta cagattggat atgcagagat ccaattgcca cagcagtcac gtcgtcagaa      540
ttctgcgtgg agcgaggaga cctcgcattc gtgcaggaaa acctgtgacg tcgagagaag      600
ttttccgcag atggagtagc tcagagacgg cgaaatcatc ttcagctgca aatcagacca      660
tattctctgg gatccagcca accggcgtag cgacacctgg aaattatctg ggagctctac      720
tggaatgggt acggctacaa aatgctgcga aggagggaac aagattgttt ttttctatcg      780
tcgacttgca tgcgttgaca gtgccacaag acgcctccca gctacgaaat tggagaaaag      840
agacatttgc aacactcatt gccgttggtt tagaccgaa tcgctcaacg attttctacc      900
agtccgccgt atgcagtatg aatatgggtt gtaaagttaa ctgaccatgt cattaggtcc      960
atgcacacgc cgaactattt tggattttgt gcacaatagc ctctatggga tatctctccc     1020
gaatgacaca gtggaaggta ataccagat caagtgccaa cctgggtcca tggtcagaag     1080
gaacagctag ctgacgtcgg ccagagcaaa ctccagttgc ctgataacgc aaatctggaa     1140
gactcgacgg cgagggtcaag gttgcgattg gggttgttct cataccctgt tctgcaggcg     1200
gcggaatatt tagttcatag gtatgctgcc caatcgttgg tacattttca cattactgat     1260
gtagatcaga gctactcatg ttcctgtcgg agatgatcaa aggcagcacc tcgaattttc     1320
gaggaacact gcgaatagtt tcaatcatgt atatggaccc attttcccgt caccagaagc     1380
aattatatgt aagtggtttt tgcctctggc ggaacgggtc tgtgttggga aattgacggc     1440
tatcaatagc gcctgctaaa cgggttatgt ccctcaaaga accgacgttg aaaatgtcca     1500
agtcccatgc cgacagacgc tcaaggatca ttcttacgga ttgcgccgca gaaatctcca     1560
aaaagatcaa tgctgcgctc acagactcgg aattaaccat tacatatgac ccagtccgtc     1620
gacctggagt ggcgaattta atagagatct tgagtcactt cgatggacga acttgcgatg     1680
agattgccat ggaataaccgt tcagccagtc ttgcgcgtct aaaggaacat ctggccagaa     1740
cgttgtccaa tcatcttgag ccaataagag agaagtatct ctacttgta ggagatcaga     1800
ctgactacct tgattctata gcagaacagg gttctgaagc cgcgcgggcc aacgctgaat     1860
tgacaatgga gcaagtcaaa gtcgctatgg gcttaattta gcccttcata tacgttgtca     1920
tcatgctccg ccgggtacac atgtaggctc agttgggtcat actctgatga tcagttcatg     1980
atggtggcca ctattgacaa ttaccacca ctattgcctg ttcagggtact actcaaacgc     2040
tgattataca atataatgca tgcatatata tctacgtgtg tgtgtgtgtg tatacatatg     2100
tatgaatatg tgcatagcta atcaaatctc gcttggggtt gtgaaagaaa tgcgacatat     2160
gcttttagaga acattctcgc ctgggattga attcatttca caaccgtata gaggtacatc     2220
atctagttat tggcagggat acgtcatcca tactggataa tggctgctgc ctacagaccc     2280
agactggtag gtatgtccac tgcgtggaga gactaaaga ggcccagctt ggtgtgcggc     2340
aagtgggagc attactagga gcatgcagtg tccttcgtac atgtaccttt tacatatgct     2400
c                                                    2401

```

<210> 100

<211> 1401

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242
Genomic sequence containing the coding region

<400> 100

atgcagagat	ccaattgcc	cagcagtc	gtcgtcagaa	ttctgcgtgg	agcgaggaga	60
cctcgcattc	gtgcaggaaa	acctgtgacg	tcgagagaag	ttttccgcag	atggagtagc	120
tcagagacgg	cgaaatcatc	ttcagctgca	aatcagacca	tattctctgg	gatccagcca	180
accggcggtac	cgcaccttgg	aaattatctg	ggagctctac	gtgaatgggt	acggctacaa	240
aatgctgcga	aggagggaac	aagattgttt	ttttctatcg	tcgacttgca	tgcgttgaca	300
gtgccacaag	acgcctccca	gctacgaaat	tggagaaaag	agacatttgc	aacactcatt	360
gccgttggtt	tagaccgaa	tcgctcaacg	atcttctacc	agtcgcgcgt	atgcagtatg	420
aatatgggtt	gtaaagttta	ctgacctatg	cattaggtcc	atgcacacgc	cgaactatct	480
tggattttgt	gcacaatagc	ctctatggga	tatctctccc	gaatgacaca	gtggaaggta	540
ataccagat	caagtgccaa	cctggtccaa	tggtcagaag	gaacagctag	ctgacgtcgg	600
ccagagcaaa	ctccagttgc	ctgataacgc	aaatctggaa	gactcgacgg	cgagggtcaag	660
gttgcgattg	gggttgttct	cataccctgt	tctgcaggcg	gcggatattc	tagttcatag	720
gtatgctgcc	caatcgttgg	tacattttca	cattactgat	gtagatcaga	gctactcatg	780
ttcctgtcgg	agatgatcaa	aggcagcacc	tcgaattttc	gaggaacact	gcgaatagtt	840
tcaatcatgt	atatggaccc	atcttcccgt	caccagaagc	aattatatgt	aagtgggttt	900
tgcttctggc	ggaacggtcc	tgtgttgagg	aattgacggc	tatcaatagc	gcctgctaaa	960
cgggttatgt	ccctcaaaga	accgacgttg	aaaatgtcca	agtcccatgc	cgacagacgc	1020
tcaaggatca	ttcttacgga	ttcgcccgc	gaaatctcca	aaaagatcaa	tgctgcgctc	1080
acagactcgg	aattaacat	tacatatgac	ccagtcgctc	gacctggagt	ggcgaattta	1140
atagagatct	tgagtcactt	cgatggacga	acttgcgatg	agattgccat	ggaataaccgt	1200
tcagccagtc	ttcgcgtctc	aaaggaacat	ctggccagaa	cggttgccaa	tcatcttgag	1260
ccaataagag	agaagtatct	ctcacttgta	ggagatcaga	ctgactacct	tgattctata	1320
gcagaacagg	gttctgaagc	cgcgcggggc	aacgctgaat	tgacaatgga	gcaagtcaaa	1380
gtcgcctatgg	gcttaattta	g				1401

<210> 101

<211> 1200

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242
Coding region without introns

<400> 101

atgcagagat	ccaattgcc	cagcagtc	gtcgtcagaa	ttctgcgtgg	agcgaggaga	60
cctcgcattc	gtgcaggaaa	acctgtgacg	tcgagagaag	ttttccgcag	atggagtagc	120
tcagagacgg	cgaaatcatc	ttcagctgca	aatcagacca	tattctctgg	gatccagcca	180
accggcggtac	cgcaccttgg	aaattatctg	ggagctctac	gtgaatgggt	acggctacaa	240
aatgctgcga	aggagggaac	aagattgttt	ttttctatcg	tcgacttgca	tgcgttgaca	300
gtgccacaag	acgcctccca	gctacgaaat	tggagaaaag	agacatttgc	aacactcatt	360
gccgttggtt	tagaccgaa	tcgctcaacg	atcttctacc	agtcgcgcgt	ccatgcacac	420
gccgaactat	tttggatttt	gtgcacaata	gcctctatgg	gatatctctc	ccgaatgaca	480
cagtgggaaga	aggaacagct	agctgacgtc	ggccagagca	aactccagtt	gcctgataac	540
gcaaactctgg	aagactcgac	ggcgaggtca	aggttgcgat	tgggggtgtt	ctcataccct	600
gttctgcagg	cggcgatat	tctaatacaga	gtactcatg	ttcctgtcgg	agatgatcaa	660
aggcagcacc	tcgaattttc	gaggaacact	gcgaatagtt	tcaatcatgt	atatggaccc	720
atcttcccgt	caccagaagc	aattatatcg	cctgctaaac	gggttatgtc	cctcaaagaa	780
ccgacgttga	aaatgtccaa	gtcccatgcc	gacagacgct	caaggatcat	tcttacggat	840
tcgcccgcag	aaatctccaa	aaagatcaat	gctgcgctca	cagactcgga	attaaccatt	900
acatatgacc	cagtcgctcg	acctggagtg	gcgaatttaa	tagagatctt	gagtcacttc	960
gatggacgaa	cttgcgatga	gattgccatg	gaataaccgt	cagccagtct	tcgcgctcta	1020

```

aaggaacatc tggccagaac gttgtccaat catcttgagc caataagaga gaagtatctc 1080
tcacttgtag gagatcagac tgactacctt gattctatag cagaacaggg ttctgaagcc 1140
gcgcggggcca acgctgaatt gacaatggag caagtcaaag tcgctatggg cttaatttag 1200

```

<210> 102

<211> 399

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242
Protein sequence

<400> 102

```

Met Gln Arg Ser Asn Cys His Ser Ser Gln Val Val Arg Ile Leu Arg
1              5              10              15

Gly Ala Arg Arg Pro Arg Ile Arg Ala Gly Lys Pro Val Thr Ser Arg
              20              25              30

Glu Val Phe Arg Arg Trp Ser Ser Ser Glu Thr Ala Lys Ser Ser Ser
              35              40              45

Ala Ala Asn Gln Thr Ile Phe Ser Gly Ile Gln Pro Thr Gly Val Pro
              50              55              60

His Leu Gly Asn Tyr Leu Gly Ala Leu Arg Glu Trp Val Arg Leu Gln
              65              70              75              80

Asn Ala Ala Lys Glu Gly Thr Arg Leu Phe Phe Ser Ile Val Asp Leu
              85              90              95

His Ala Leu Thr Val Pro Gln Asp Ala Ser Gln Leu Arg Asn Trp Arg
              100             105             110

Lys Glu Thr Phe Ala Thr Leu Ile Ala Val Gly Leu Asp Pro Asn Arg
              115             120             125

Ser Thr Ile Phe Tyr Gln Ser Ala Val His Ala His Ala Glu Leu Phe
              130             135             140

Trp Ile Leu Cys Thr Ile Ala Ser Met Gly Tyr Leu Ser Arg Met Thr
              145             150             155             160

Gln Trp Lys Lys Glu Gln Leu Ala Asp Val Gly Gln Ser Lys Leu Gln
              165             170             175

Leu Pro Asp Asn Ala Asn Leu Glu Asp Ser Thr Ala Arg Ser Arg Leu
              180             185             190

Arg Leu Gly Leu Phe Ser Tyr Pro Val Leu Gln Ala Ala Asp Ile Leu
              195             200             205

Ile Arg Ala Thr His Val Pro Val Gly Asp Asp Gln Arg Gln His Leu
              210             215             220

Glu Phe Ser Arg Asn Thr Ala Asn Ser Phe Asn His Val Tyr Gly Pro
              225             230             235             240

```


Ile Phe Pro Ser Pro Glu Ala Ile Ile Ser Pro Ala Lys Arg Val Met
 245 250 255

Ser Leu Lys Glu Pro Thr Leu Lys Met Ser Lys Ser His Ala Asp Arg
 260 265 270

Arg Ser Arg Ile Ile Leu Thr Asp Ser Pro Ala Glu Ile Ser Lys Lys
 275 280 285

Ile Asn Ala Ala Leu Thr Asp Ser Glu Leu Thr Ile Thr Tyr Asp Pro
 290 295 300

Val Arg Arg Pro Gly Val Ala Asn Leu Ile Glu Ile Leu Ser His Phe
 305 310 315 320

Asp Gly Arg Thr Cys Asp Glu Ile Ala Met Glu Tyr Arg Ser Ala Ser
 325 330 335

Leu Arg Ala Leu Lys Glu His Leu Ala Arg Thr Leu Ser Asn His Leu
 340 345 350

Glu Pro Ile Arg Glu Lys Tyr Leu Ser Leu Val Gly Asp Gln Thr Asp
 355 360 365

Tyr Leu Asp Ser Ile Ala Glu Gln Gly Ser Glu Ala Ala Arg Ala Asn
 370 375 380

Ala Glu Leu Thr Met Glu Gln Val Lys Val Ala Met Gly Leu Ile
 385 390 395

<210> 103

<211> 3805

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 103

cacccatttt	gtagtaattc	tcgagaaatc	cgctctgaat	acccaccagg	ggaaagatgt	60
caattatcac	tatgagaaac	aaaaggctgc	tattttacct	cttcgggacg	tggtggacgc	120
gtcgcggggc	atgctatgtt	tgtcctgttt	gcaccaaaca	ggaattgccg	taaaatggga	180
acagagtttg	ttagctcacc	gcctttggat	tttcaactgt	aaaacaaaaa	aaaagtgaga	240
tttaccatca	cgacagggct	ggatctgttc	tggtcggaaag	gagacggcag	gcgatttgga	300
tttctatttc	gcccttgcaa	agtaattgga	tgcaaagggt	tctgtgttct	attttgcgtc	360
ttgcaacttg	atggaattcg	aagcctgagc	tgtcctgagc	ttcaaaatat	cttctctcgc	420
cctcggggcg	cctcaaacca	cttttctttc	ccatattttg	tttgagcgcg	cctgcgccag	480
ctgcgcaaca	gagttccaag	atgcctcacc	gcgcggcacc	cccagcgggt	tcggaaaatg	540
agttcgacat	cacaggcgct	ctcttccaga	acgacagcga	ctccgacaac	gaacagccct	600
cggccaagtc	caaacgacaa	cctccgaaga	aggttccctc	gcaggcgctc	gacttcctcg	660
gcgatgtgaa	tgaagacgac	aatgacgacg	aggcttttat	tgccgagcag	caaacttctg	720
ccaaccgcaa	ggcctcgaat	ctcaaaggtc	gcactgttaa	gaagggtggt	ggtttccaag	780
ccatgggctt	gagtgcgaat	ctgttaaagg	caatcgctcg	gaaaggcttc	tcggtaccga	840
ctcccattca	gcgcaagacc	attcccgtta	ttatggacga	ccaggatgta	gttggtatgg	900
cacggactgg	ttcaggaaaag	acggccgctt	tcgttatccc	aatgatcgag	aaattgaaga	960
gccatagcac	caagggttga	gcccgcggtc	tggtcttgtc	cccacgcaga	gagctggcac	1020
tgcagacatt	gaaagtcgtc	aaggaactgg	gtagaggcac	tgacctgaag	tcggttcttc	1080
ttgttggtgg	agacagcctg	gaggagcaat	tcgcgatgat	cgccggcaat	ccagatatta	1140
ttattgcaac	acctggtcga	ttcctgcatt	tgaagggtga	aatgaacctg	gacttgtcca	1200

gtatccgcta	tgtcgttttc	gacgaggctg	atcgactggt	tgagatgggt	ttcgccgcgc	1260
aactaacaga	gattttgcac	ggtcttcctg	cgaatcggca	gactctcctg	ttctctgcca	1320
ctcttccgaa	gtcccttgtc	gagtttgccc	gcgcgggctt	gcaggaacct	acactagtc	1380
gtctggatac	cgagagcaag	atctcgccc	atcttcagaa	tgctttcttc	tctgtgaaat	1440
cctcagagaa	ggaaggggcc	ttgctctaca	tccttcatga	ggtcatcaag	atgccgactg	1500
ggccaaccga	ggtttcgcaa	caaaggaaag	aagaagatgc	aagcgccaag	aacttgaaga	1560
acaagaagag	gaagagagcg	gaaatggaga	aggctgtcaa	tacgagagag	tctccaacca	1620
agcattcgac	aatcgttttt	gccgcgacga	agcaccatgt	cgattatctt	tactcactac	1680
tctgcgaggc	gggattcgcc	gtctcctacg	tttacggctc	tttagatcaa	accgcccga	1740
agatccaggt	tcaaaacttt	agaacgggca	tgaccaatat	cctcgttgtc	accgacgttg	1800
cggctagagg	tattgatatt	cctatccttg	caaattgtcat	taattacgat	ttcccctccc	1860
agccaaagat	ttttgttcac	cggtcgggcc	gaactgctcg	tgccgggcgc	aagggctgga	1920
gttacagtct	ggtccgcat	gcagacgctc	cttatttact	tgatttgcaa	ctattcctag	1980
gaagaaggct	ggttggtggc	cgcgaattcg	gggatcaagt	gaacttcgcc	gaagacgttg	2040
taacgggcag	tctacctagg	gatgggctct	ctcaaagctg	tgagtgggta	accaaggtcc	2100
tggacgataa	tgcagacctt	gcagcccaac	gcacggctcg	tgctaagggt	gagaagctct	2160
atatgcgaac	ccggaacgcg	gcattctctt	agagtgcgaa	gcgatcga	caggtggttt	2220
cttccgacaa	ttggacaagc	gtacaccgcg	tcttccaaga	tgaaactagt	aatctggagg	2280
ccgagcggga	gaagatgctc	gcccgtattg	gtggttaccg	gccgccagag	acaatctttg	2340
aggtcaacaa	ccggcggatg	ggcaaacatg	agaacgtcga	cgctctcgat	acgattaaga	2400
gagttcgtag	cactctagag	tccaagaaga	agcgtgcaca	agcgaatgaa	aagtccgagt	2460
tcctcgaa	cggtcccagc	gacggaaagg	cagtcaacga	agccaaagaa	accgagagcg	2520
agggagcatt	ttctgatgag	gacgacgacg	ttcccaccgg	cgtggcagat	aacatgtcga	2580
tggcatccga	ttcagagctg	gaagtcacct	tctcgtcata	ttcaaaatca	aaggacaaca	2640
aggcgaagaa	agcgagcgcg	gcattctttc	agaaccctga	atacttcatg	tcctataccc	2700
cgaataacac	ctccctggcg	gaggaccgag	cttatggtgt	gcattccggt	accaactcca	2760
acttcgcccc	ggcctcacgc	agcgcgacca	tggatctggc	aggcgacgat	ggaggccgcg	2820
ggttcggcga	ggctcgtacg	ctgatgcgct	gggacaagcg	acacaagaag	tacgtggctc	2880
gacagaatga	cgaggacggc	tccaagggca	cacgcctcgt	ccgcggtgag	agcggggcga	2940
agatcgacgc	cagcttccgg	agcggagcgt	tcgacgcttg	gaagagagaa	aatcgtctcg	3000
gccgcttgcc	tcgggtgggt	gaggccgaag	ctgctaattc	cgctgctggt	ctcaacgcag	3060
ccatctcagg	caagcgggtt	aggcatcgca	aggagcaggc	gccaagaag	gctgatcctc	3120
tccgtgggtga	ttacgagaag	atgaagaaga	aggctgaact	cgccaaggag	cgagcaatgt	3180
ctaaggctgg	cggcgctgca	ccacgtggca	agagcgagct	gaagagtacg	gacgatatcc	3240
ggattgcgcg	caaattgaag	cagaagagac	gagagaagaa	tgctcgtccc	tcgaggaaga	3300
agtaaccggg	agggttaattt	tcagagttat	gtatatacca	ggaattgcct	atgatacctg	3360
ctactgtgta	attttttttt	atactaaagc	ccaatccaaa	acactcttgg	gaacgaccga	3420
ggccaaacat	tcctgggtgac	agagattacc	tttcagcact	tatgccaaac	cacaaagctc	3480
tctcagtaaa	accgccaata	cgttaacacc	cctccaatac	tccgtacagc	agctctcatc	3540
gcattcactga	gaaaatgtcg	cttgatatct	tacccaacag	tgaagaagac	ccacagaccc	3600
aagccgaaaa	tttcaagggtg	accggaattt	tctcggccgc	aaagggagaa	caagatagaa	3660
tgcaaatgga	cgatctccca	atctccatca	gctggactat	tgattccgac	ggtgaatagt	3720
ggagcatctg	tgctgcgcta	ttgggttctc	cgtgacgcgc	ctcctttggt	gactcgtttt	3780
ctttgctttt	tccttcagca	cttgg				3805

<210> 104

<211> 2805

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350
Genomic sequence containing the coding region

<400> 104

atgcctcacc	gcgcggcatc	cccagcgggtg	tcggaaaatg	agttcgacat	cacaggcgct	60
ctcttccaga	acgacagcga	ctccgacaac	gaacagccct	cggccaagtc	caaacgacaa	120
cctccgaaga	aggttccctc	gcaggcgctc	gacttcctcg	gcgatgtgaa	tgaagacgac	180
aatgacgagc	aggcttttat	tgccgagcag	caaacttctg	ccaaccgcaa	ggcctcgaat	240
ctcaaaggctc	gcactgttaa	gaaggggtgt	ggtttccaag	ccatgggctt	gagtgccaat	300

ctgttaaagg	caatcgctcg	gaaaggcttc	tcggtaccga	ctcccattca	gcgcaagacc	360
attcccgtta	ttatggacga	ccaggatgta	gttggatatg	cacggactgg	ttcaggaaag	420
acggccgctt	tcgttatccc	aatgatcgag	aaattgaaga	gccatagcac	caaggttgga	480
gcccgcggtc	tggtcttgtc	cccatcgaga	gagctggcac	tgcagacatt	gaaagtcgtc	540
aagggaactgg	gtagaggcac	tgacctgaag	tcggttcttc	ttgttggtgg	agacagcctg	600
gaggagcaat	tcgcgatgat	cgccggcaat	ccagatatta	ttattgcaac	acctggtcga	660
ttcctgcatt	tgaagggtgga	aatgaacctg	gacttggtcca	gtatccgcta	tgctggtttc	720
gacgaggctg	atcgactggt	tgagatgggt	ttcgccgcgc	aactaacaga	gattttgcac	780
gggtcttctg	cgaatcggca	gactctcctg	ttctctgcca	ctcttccgaa	gtcccttgct	840
gagtttgccc	gcgcccggctt	gcaggaacct	acactagtcc	gtctggatac	cgagagcaag	900
atctcgccc	atcttcagaa	tgctttcttc	tctgtgaaat	cctcagagaa	ggaaggggccc	960
ttgctctaca	tcttcataga	ggtcatcaag	atgccgactg	ggccaaccga	ggtttcgcaa	1020
caaaggaaag	aagaagatgc	aagcgccaag	aacttgaaga	acaagaagag	gaagagagcg	1080
gaaatggaga	aggctgtcaa	tacgagagag	tctccaacca	agcattcgac	aatcgttttt	1140
gccgcgacga	agcaccatgt	cgattatctt	tactcactac	tctgcgaggc	gggattcgcc	1200
gtctctacg	tttacggctc	tttagatcaa	accgcccga	agatccagggt	tcaaaacttt	1260
agaacgggca	tgaccaatat	cctcgttgct	accgacgttg	cggttagagg	tattgatatt	1320
cctatcctgg	caaagtgtcat	taattacgat	ttcccctccc	agccaaagat	ttttgttcac	1380
cgtgtcggcc	gaactgctcg	tgccggggcg	aagggtcgga	gttacagtct	ggtccgcgat	1440
gcagacgctc	cttatttact	tgatttgcaa	ctattcctag	gaagaaggct	ggttggtggc	1500
cgcgaattcg	gggatcaagt	gaacttcgcc	gaagacgttg	taacggggcag	tctacctagg	1560
gatgggtctc	ctcaaagctg	tgagtgggta	accaaggtcc	tggaacgataa	tgacacctt	1620
gcagcccaac	gcacggtcgc	tgctaagggt	gagaagctct	atatgcgaac	ccggaacgcg	1680
gcatctcttg	agagtgcgaa	gcgatcgaaa	caggtgggtt	cttccgacaa	ttggacaagc	1740
gtacacccgc	tcttccaaga	tgaaactagt	aatctggagg	ccgagcggga	gaagatgctc	1800
gcccgtattg	gtggttaccg	gccgccagag	acaatctttg	aggtcaacaa	ccggcggatg	1860
ggcaaacatg	agaacgtcga	cgctctcgat	acgattaaga	gagttcgtag	cactctagag	1920
tccaagaaga	agcgtgcaca	agcgaatgaa	aagtcggagt	tctcgaaga	cggtcccgc	1980
gacggaaagg	cagtcacga	agccaaagaa	accgagagcg	agggagcatt	ttctgatgag	2040
gacgacgacg	ttcccaccgg	cgtggcagat	aacatgtcga	tggtcatccga	ttcagagctg	2100
gaagtcacct	tctcgtcata	ttcaaaatca	aaggacaaca	aggcgaagaa	agcgagcgcg	2160
gcatctttcc	agaaccctga	atacttcatg	tctataccc	cgaataacac	ctccctggcg	2220
gaggaccgag	cttatgggtg	gcattccggg	accaactcca	acttcgccca	ggcctcacgc	2280
agcgcgacca	tggatctggc	aggcgacgat	ggaggccgcg	ggttcggcga	ggctcgtacg	2340
ctgatgcgct	gggacaagcg	acacaagaag	tacgtggctc	gacagaatga	cgaggacggc	2400
tccaagggca	cacgcctcgt	ccgcgggtgag	agcggggcga	agatcgcagc	cagcttccgg	2460
agcggacggt	tcgacgcttg	gaagagagaa	aatcgtctcg	gccgcttgcc	tcgggtgggt	2520
gaggccgaag	ctgctaactc	cgctgctggt	ctcaacgcag	ccatctcagg	caagcggttc	2580
aggcatcgca	aggagcaggc	gccaagaag	gctgatcctc	tccgtgggtga	ttacgagaag	2640
atgaagaaga	aggctgaact	cgccaaggag	cgagcaatgt	ctaaggctgg	cggcgctgca	2700
ccacgtggca	agagcgagct	gaagagtacg	gacgatatcc	ggattgcgcg	caaattgaag	2760
cagaagagac	gagagaagaa	tgctcgtccc	tcgaggaaga	agtaa		2805

<210> 105

<211> 2805

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350

Coding region without introns

<400> 105

atgcctcacc	gcgcggcatc	cccagcgggtg	tcggaaaatg	agttcgacat	cacaggcgct	60
ctcttccaga	acgacagcga	ctccgacaac	gaacagccct	cggccaagtc	caaacgacaa	120
cctccgaaga	aggttccctc	gcaggcgctc	gacttctctg	gcgatgtgaa	tgaagacgac	180
aatgacgacg	aggcttttat	tgccgagcag	caaacttctg	ccaaccgcaa	ggcctcgaat	240
ctcaaaggtc	gcactgttaa	gaagggtggt	ggtttccaag	ccatgggctt	gagtgccaat	300
ctgttaaagg	caatcgctcg	gaaaggcttc	tcggtaccga	ctcccattca	gcgcaagacc	360
attcccgtta	ttatggacga	ccaggatgta	gttggatatg	cacggactgg	ttcaggaaag	420

```

acggccgctt tcgttatccc aatgatcgag aaattgaaga gccatagcac caaggttggg 480
gccccgggtc tgggtctgtc cccatcgaga gagctggcac tgcagacatt gaaagtcgtc 540
aaggaactgg gtagaggcac tgacctgaag tcggttcttc ttgttgggtg agacagcctg 600
gaggagcaat tcgcgatgat cgccggcaat ccagatatta ttattgcaac acctggtcga 660
ttcctgcatt tgaagggtga aatgaacctg gacttgtcca gtatccgcta tgtcgttttc 720
gacgaggctg atcgactggt tgagatgggt ttccgcccgc aactaacaga gattttgcac 780
ggtcttctct cgaatcggca gactctctct ttctctgcca ctcttccgaa gtcccttgtc 840
gagtttgccc gcgcccggct gcaggaacct acactagtcc gtctggatac cgagagcaag 900
atctcgcccc atcttcagaa tgctttcttc tctgtgaaat cctcagagaa ggaagggggc 960
ttgctctaca tccttcatga ggtcatcaag atgccgactg ggccaaccga ggtttcgcaa 1020
caaaggaaa aagaagatgc aagcgccaag aacttgaaga acaagaagag gaagagagcg 1080
gaaatggaga aggtctgtcaa tacgagagag tctccaacca agcattcgac aatcgttttt 1140
gccgcgacga agcaccatgt cgattatctt tactcactac tctgcgaggg gggattcgcc 1200
gtctcctacg tttacggctc tttagatcaa accgcccga agatccaggt tcaaaacttt 1260
agaacgggca tgaccaatat cctcgttggt accgacgttg cggctagagg tattgatatt 1320
cctatcctgg caaatgtcat taattacgat ttcccctccc agccaaagat ttttgttcac 1380
cgtgtcggcc gaactgctcg tgccggggcg aagggctgga gttacagtct ggtcccgcat 1440
gcagacgctc cttattttact tgatttgcaa ctattcctag gaagaaggct ggttggtggc 1500
cgcgaaattcg gggatcaagt gaacttcgcc gaagacgttg taacgggcag tctacctagg 1560
gatgggctct ctcaaagctg tgagtgggta accaaggctc tggacgataa tgcagacctt 1620
gcagcccaac gcacggctcg tgctaagggt gagaagctct atatgcgaac ccggaacgcg 1680
gcattctctt agagtgcgaa gcgatcgaaa cagggtggtt ctccgcgaaa ttggacaagc 1740
gtacaccgct tcttccaaga tgaaactagt aatctggagg ccgagcggga gaagatgctc 1800
gcccgtattg gtggttaccg gccgccagag acaatctttg aggtcaacaa ccggcggtatg 1860
ggcaaacatg agaacgtcga cgctctcgat acgattaaga gagttcgtag cactctagag 1920
tccaagaaga agcgtgcaca agcgaatgaa aagtccgagt tcctcgaaga cggccccgac 1980
gacggaaaag cagtcaacga agccaaagaa accgagagcg agggagcatt ttctgatgag 2040
gacgacgacg ttcccaccgg cgtggcagat aacatgtcga tggcatccga ttcagagctg 2100
gaagtcacct tctcgtcata ttcaaaatca aaggacaaca aggcgaagaa agcgagcgcg 2160
gcattcttcc agaaccctga atacttcatg tcctataccc cgaataaacac ctccctggcg 2220
gaggaccgag cttatggtgt gcattccggt accaactcca acttcgcca ggctcacgc 2280
agcgcgacca tggatctggc aggcgacgat ggaggccgcg ggttcggcga ggctcgtacg 2340
ctgatgcgct gggacaagcg acacaagaag tacgtggctc gacagaatga cgaggacggc 2400
tccaagggca cacgcctcgt ccgcggtgag agcggggcga agatcgcagc cagcttcggg 2460
agcggacggt tcgacgcttg gaagagagaa aatcgtctcg gccgcttgcc tcgggtgggt 2520
gaggccgaag ctgctaactc cgctgctggt ctcaacgcag ccatctcagg caagcggttc 2580
aggcatcgca aggagcaggc gcccaagaag gctgatctc tccgtggtga ttacgagaag 2640
atgaagaaga aggtgaact cgccaaggag cgagcaatgt ctaaggctgg cggcgctgca 2700
ccacgtggca agagcgagct gaagagtacg gacgatatcc ggattgcgcg caaattgaag 2760
cagaagagac gagagaagaa tgctcgtccc tcgaggaaga agtaa 2805

```

<210> 106

<211> 934

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350
Protein sequence

<400> 106

```

Met Pro His Arg Ala Ala Ser Pro Ala Val Ser Glu Asn Glu Phe Asp
1           5           10           15

```

```

Ile Thr Gly Ala Leu Phe Gln Asn Asp Ser Asp Ser Asp Asn Glu Gln
          20           25           30

```

```

Pro Ser Ala Lys Ser Lys Arg Gln Pro Pro Lys Lys Val Pro Ser Gln
          35           40           45

```

Ala Leu Asp Phe Leu Gly Asp Val Asn Glu Asp Asp Asn Asp Asp Glu
 50 55 60
 Ala Phe Ile Ala Glu Gln Gln Thr Ser Ala Asn Arg Lys Ala Ser Asn
 65 70 75 80
 Leu Lys Gly Arg Thr Val Lys Lys Gly Gly Gly Phe Gln Ala Met Gly
 85 90 95
 Leu Ser Ala Asn Leu Leu Lys Ala Ile Ala Arg Lys Gly Phe Ser Val
 100 105 110
 Pro Thr Pro Ile Gln Arg Lys Thr Ile Pro Val Ile Met Asp Asp Gln
 115 120 125
 Asp Val Val Gly Met Ala Arg Thr Gly Ser Gly Lys Thr Ala Ala Phe
 130 135 140
 Val Ile Pro Met Ile Glu Lys Leu Lys Ser His Ser Thr Lys Val Gly
 145 150 155 160
 Ala Arg Gly Leu Val Leu Ser Pro Ser Arg Glu Leu Ala Leu Gln Thr
 165 170 175
 Leu Lys Val Val Lys Glu Leu Gly Arg Gly Thr Asp Leu Lys Ser Val
 180 185 190
 Leu Leu Val Gly Gly Asp Ser Leu Glu Glu Gln Phe Ala Met Ile Ala
 195 200 205
 Gly Asn Pro Asp Ile Ile Ile Ala Thr Pro Gly Arg Phe Leu His Leu
 210 215 220
 Lys Val Glu Met Asn Leu Asp Leu Ser Ser Ile Arg Tyr Val Val Phe
 225 230 235 240
 Asp Glu Ala Asp Arg Leu Phe Glu Met Gly Phe Ala Ala Gln Leu Thr
 245 250 255
 Glu Ile Leu His Gly Leu Pro Ala Asn Arg Gln Thr Leu Leu Phe Ser
 260 265 270
 Ala Thr Leu Pro Lys Ser Leu Val Glu Phe Ala Arg Ala Gly Leu Gln
 275 280 285
 Glu Pro Thr Leu Val Arg Leu Asp Thr Glu Ser Lys Ile Ser Pro Asp
 290 295 300
 Leu Gln Asn Ala Phe Phe Ser Val Lys Ser Ser Glu Lys Glu Gly Ala
 305 310 315 320
 Leu Leu Tyr Ile Leu His Glu Val Ile Lys Met Pro Thr Gly Pro Thr
 325 330 335
 Glu Val Ser Gln Gln Arg Lys Glu Glu Asp Ala Ser Ala Lys Asn Leu
 340 345 350
 Lys Asn Lys Lys Arg Lys Arg Ala Glu Met Glu Lys Ala Val Asn Thr
 355 360 365

Arg Glu Ser Pro Thr Lys His Ser Thr Ile Val Phe Ala Ala Thr Lys
 370 375 380
 His His Val Asp Tyr Leu Tyr Ser Leu Leu Cys Glu Ala Gly Phe Ala
 385 390 395 400
 Val Ser Tyr Val Tyr Gly Ser Leu Asp Gln Thr Ala Arg Lys Ile Gln
 405 410 415
 Val Gln Asn Phe Arg Thr Gly Met Thr Asn Ile Leu Val Val Thr Asp
 420 425 430
 Val Ala Ala Arg Gly Ile Asp Ile Pro Ile Leu Ala Asn Val Ile Asn
 435 440 445
 Tyr Asp Phe Pro Ser Gln Pro Lys Ile Phe Val His Arg Val Gly Arg
 450 455 460
 Thr Ala Arg Ala Gly Arg Lys Gly Trp Ser Tyr Ser Leu Val Arg Asp
 465 470 475 480
 Ala Asp Ala Pro Tyr Leu Leu Asp Leu Gln Leu Phe Leu Gly Arg Arg
 485 490 495
 Leu Val Val Gly Arg Glu Phe Gly Asp Gln Val Asn Phe Ala Glu Asp
 500 505 510
 Val Val Thr Gly Ser Leu Pro Arg Asp Gly Leu Ser Gln Ser Cys Glu
 515 520 525
 Trp Val Thr Lys Val Leu Asp Asp Asn Ala Asp Leu Ala Ala Gln Arg
 530 535 540
 Thr Val Ala Ala Lys Gly Glu Lys Leu Tyr Met Arg Thr Arg Asn Ala
 545 550 555 560
 Ala Ser Leu Glu Ser Ala Lys Arg Ser Lys Gln Val Val Ser Ser Asp
 565 570 575
 Asn Trp Thr Ser Val His Pro Leu Phe Gln Asp Glu Thr Ser Asn Leu
 580 585 590
 Glu Ala Glu Arg Glu Lys Met Leu Ala Arg Ile Gly Gly Tyr Arg Pro
 595 600 605
 Pro Glu Thr Ile Phe Glu Val Asn Asn Arg Arg Met Gly Lys His Glu
 610 615 620
 Asn Val Asp Ala Leu Asp Thr Ile Lys Arg Val Arg Ser Thr Leu Glu
 625 630 635 640
 Ser Lys Lys Lys Arg Ala Gln Ala Asn Glu Lys Ser Glu Phe Leu Glu
 645 650 655
 Asp Gly Pro Asp Asp Gly Lys Ala Val Asn Glu Ala Lys Glu Thr Glu
 660 665 670
 Ser Glu Gly Ala Phe Ser Asp Glu Asp Asp Asp Val Pro Thr Gly Val
 675 680 685
 Ala Asp Asn Met Ser Met Ala Ser Asp Ser Glu Leu Glu Val Thr Phe

690	695	700
Ser Ser Tyr Ser Lys	Ser Lys Asp Asn Lys	Ala Lys Lys Ala Ser Ala
705	710	715 720
Ala Ser Phe Gln Asn	Pro Glu Tyr Phe Met	Ser Tyr Thr Pro Asn Asn
	725	730 735
Thr Ser Leu Ala Glu	Asp Arg Ala Tyr Gly	Val His Ser Gly Thr Asn
	740	745 750
Ser Asn Phe Ala Gln	Ala Ser Arg Ser Ala	Thr Met Asp Leu Ala Gly
	755	760 765
Asp Asp Gly Gly Arg	Gly Phe Gly Glu Ala	Arg Thr Leu Met Arg Trp
	770	775 780
Asp Lys Arg His Lys	Lys Tyr Val Ala Arg	Gln Asn Asp Glu Asp Gly
	785	790 795 800
Ser Lys Gly Thr Arg	Leu Val Arg Gly Glu	Ser Gly Ala Lys Ile Ala
	805	810 815
Ala Ser Phe Arg Ser	Gly Arg Phe Asp Ala	Trp Lys Arg Glu Asn Arg
	820	825 830
Leu Gly Arg Leu Pro	Arg Val Gly Glu Ala	Glu Ala Ala Asn Leu Ala
	835	840 845
Ala Gly Leu Asn Ala	Ala Ile Ser Gly Lys	Arg Phe Arg His Arg Lys
	850	855 860
Glu Gln Ala Pro Lys	Lys Ala Asp Pro Leu	Arg Gly Asp Tyr Glu Lys
	865	870 875 880
Met Lys Lys Lys Ala	Glu Leu Ala Lys Glu	Arg Ala Met Ser Lys Ala
	885	890 895
Gly Gly Ala Ala Pro	Arg Gly Lys Ser Glu	Leu Lys Ser Thr Asp Asp
	900	905 910
Ile Arg Ile Ala Arg	Lys Leu Lys Gln Lys	Arg Arg Glu Lys Asn Ala
	915	920 925
Arg Pro Ser Arg Lys	Lys	
	930	

<210> 107

<211> 2413

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 107

cctcctcttc	ttccactgcc	tcatcatcac	ggatatggatt	gtcatcagcc	atagtgagaa	60
tagtgaatgg	gtttagaagt	tacagcctag	aaatgagagg	gaaagagagg	tacattgaaa	120
gcaagaagat	atggtcggta	tttacatcac	ctccttctct	gccttgagtg	cctaccgctc	180

tgctgcctgc	gtgcccaccg	acttcaccag	tgacgcgac	tcgtcatcgg	agcaacgcgg	240
gggaaacacg	aacatcacgt	gaatgcgcca	agacttgatg	accccaaatt	attactgatt	300
ggtcaaactt	ccagcactgt	tccgtcatca	accacctaag	ggcctagata	tggtctccag	360
ttacagatcc	ttcgtgccac	gattctttca	ttgagtggtc	aaatactact	cgacgtattt	420
ttgtgggctt	cagtttgtgg	ctaagttag	accgatagac	gacggccaac	ctttttaata	480
cactatcadc	gcacctcccc	atggctctcc	gccggccatt	aacacttccg	aggcacattc	540
tcaatggagc	ttgttttaggc	ttgcgaccag	ctgtgtctcg	cgccgctctg	gcttatgggc	600
aggagcagag	gaaagggctt	gcaacagcag	ttcccccggt	cactcaaaat	gcggctgggt	660
ccaaaggccc	cacggcaatg	gtcttcctca	acatgggtgg	gccatcgaag	attgacgaag	720
tggaagattt	tctgagcaga	ttatttgtat	gcattcctca	atatgcccg	tgctaccacc	780
atgtatgagt	ctgacaaact	ctctcttctt	ataccaggcc	gatggcgatc	tgattcctct	840
cggacgactt	caatcatacc	tcggccctct	catcgctaag	cgcagaaccc	caaagatcca	900
acggcaatac	tcggatattg	gtggagggtc	accgatcagg	aaatgggtccg	agtatcagtg	960
cgaggaaatg	tgacagattgc	tagacaaaat	caatcccgaa	acggctcctc	acaagcctta	1020
cgctcgcttc	cggtacgccc	accctctgac	ggaagaaatg	tacacaaagt	tgctggaaga	1080
tggattcggc	aacgggaaag	gcgggcgcgc	tgctcgcttc	acacagtacc	cccaatattc	1140
gtgctccacc	acgggtagct	cgctgaacga	gttggtgaaa	tgagagaacca	ggcttgaggg	1200
taagcgtgca	aatggcaaca	tggacccgcg	tgggtccatc	cagtggagtg	tcattgatcg	1260
atggccaacg	caccctggcc	tcgtggaggg	tttcgcccgg	aacattgagg	agcagctgaa	1320
gacataccca	gaggagaagc	gaaacgggtg	cgctctcttg	ttctcagccc	acagtctgcc	1380
catgagtgtt	gtcaacagag	gtgagactca	tcttcttacc	gaacaacaag	atttgctcgc	1440
taacacattt	cctaggcgac	ccatatacctg	ctgaagtgtg	tgcaactgtg	catgctgtca	1500
tgcaaaagatt	gaatttcagc	aatccttacc	gactgtgctg	gcagtcccaa	gtgggaccgt	1560
cagcttggtt	tggagcccaa	actagcgata	cggctcgaaa	ctatgtcaaa	cgtggacaga	1620
ccgatattat	tctagttccc	attgccttca	ccagcgacca	tattgagact	ctgtacgagt	1680
tggatctgga	agtgataaag	gaagcaaact	ccccgggagt	caagagagcc	gagagtittga	1740
atggtaaccc	cattttcatt	caggcattag	cagacattgc	ccaagagcac	ctccgtaagg	1800
gagagaagtg	ctcactacag	atgactctgc	gctgtcaagg	ctgtaagagc	gaacgggtgc	1860
tggaaacagaa	gaaattcttt	gctggcgacc	gattttcttc	tcttgtagtt	tagtgatatt	1920
ctatatggct	gttctctgcc	gttgatataca	atactagggg	ccattttctt	tcttcagggc	1980
gttaagtgtg	gttgatcaacg	aggtgaccca	ttcacggagc	acagcagagc	aatgtatata	2040
ttgttgaaaa	agtccaagca	tataatctca	tttcgttggt	ggctctcaat	ggttgagaat	2100
atataaaaatc	attaggaatg	aaggatttcc	gggtcaacct	ttgacaatta	ttttgccacc	2160
atttaacggt	gcacatatgc	aacgataaag	cacgacccag	tcgtagtgtt	ggtgtccctt	2220
atcgagaaat	tgcatgagat	tactccaacc	gctcaaaaatc	tcaaaccctg	ataagaaaaa	2280
ttgattattg	aacaaactct	catagcgtcg	tttcgttaatt	actggttggt	cggaatcggg	2340
ctgacgcaaa	gccaacggc	cacgaagctg	ctccagctcc	gttcccagtt	ctcgtgaaga	2400
attggtaatc	atg					2413

<210> 108

<211> 1413

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420
Genomic sequence containing the coding region

<400> 108

atggctctcc	gccggccatt	aacacttccg	aggcacattc	tcaatggagc	ttgttttaggc	60
ttgcgaccag	ctgtgtctcg	cgccgctctg	gcttatgggc	aggagcagag	gaaagggctt	120
gcaacagcag	ttcccccggt	cactcaaaat	gcggctgggt	ccaaaggccc	cacggcaatg	180
gtcttctctca	acatgggttg	gccatcgaa	attgacgaag	tggaagattt	tctgagcaga	240
ttatttgtat	gcattcctca	atatgcccg	tgctaccacc	atgtatgagt	ctgacaaact	300
ctctcttctt	ataccaggcc	gatggcgatc	tgattcctct	cggacgactt	caatcatacc	360
tcggccctct	catcgctaag	cgcagaaccc	caaagatcca	acggcaatac	tcggatattg	420
gtggagggtc	accgatcagg	aaatgggtccg	agtatcagtg	cgaggaaatg	tgacagattgc	480
tagacaaaat	caatcccgaa	acggctcctc	acaagcctta	cgctcgcttc	cggtacgccc	540
accctctgac	ggaagaaatg	tacacaaagt	tgctggaaga	tggattcggc	aacgggaaag	600
gcgggcgcgc	tgctcgcttc	acacagtacc	cccaatattc	gtgctccacc	acgggtagct	660

cgctgaacga	gttgtggaaa	tggagaacca	ggcttgaggg	taagcgtgca	aatggcaaca	720
tggaccccg	tggtgccatc	cagtggagtg	tcattgatcg	atggccaacg	caccctggcc	780
tcggtggagg	tttcgcccgg	aacattgagg	agcagctgaa	gacataccca	gaggagaagc	840
gaaacgggtg	cgttctcttg	ttctcagccc	acagtctgcc	catgagtgtt	gtcaacagag	900
gtgagactca	tcttcttacc	gaacaacaag	atttgctcgc	taacacattt	cctaggcgac	960
ccatatactg	ctgaagttgc	tgcaactgtg	catgctgtca	tgcaaagatt	gaatttcagc	1020
aatccttacc	gactgtgctg	gcagtcccaa	gtgggaccgt	cagcttggct	tggagcccaa	1080
actagcgata	cggtcgaaaa	ctatgtcaaa	cgtggacaga	ccgatattat	tctagttccc	1140
attgccttca	ccagcgacca	tattgagact	ctgtacgagt	tggatctgga	agtgataaag	1200
gaagcaaaact	ccccgggagt	caagagagcc	gagagtttga	atggtaacct	cattttcatt	1260
caggcattag	cagacattgc	ccaagagcac	ctccgtaagg	gagagaagtg	ctcactacag	1320
atgactctgc	gctgtcaagg	ctgttaagag	gaacggtgcc	tggaaacagaa	gaaattcttt	1380
gctggcgacc	gattttcttc	tctttagatt	tag			1413

<210> 109

<211> 1287

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420
Coding region without introns

<400> 109						
atggctctcc	gccggccatt	aacacttccg	aggcacattc	tcaatggagc	ttgttttaggc	60
ttgcgaccag	ctgtgtctcg	cgccgctctg	gcttatgggc	aggagcagag	gaaagggctt	120
gcaacagcag	ttcccccggt	caactcaaaat	gcggctgggt	ccaaaggccc	cacggcaatg	180
gtcttctcct	acatgggtgg	gccatcgaag	attgacgaag	tggaaagattt	tctgagcaga	240
ttatttgccg	atggcgatct	gattcctctc	ggacgacttc	aatcatacct	cgccctctc	300
atcgctaagc	gcagaacccc	aaagatccaa	cggcaatact	cggatattgg	tggagggtca	360
ccgatcagga	aatggtccga	gtatcagtgc	gaggaaatgt	gcagattgct	agacaaaatc	420
aatcccga	cggtcctca	caagccttac	gtcgcgttcc	ggtacgccga	ccctctgacg	480
gaagaaatgt	acacaaagtt	gctggaagat	ggattcggca	acgggaaagg	cgggcgcgct	540
gtcgcgttca	cacagtaccc	ccaatattcg	tgtccacca	cgggtagctc	gctgaacgag	600
ttgtggaaat	ggagaaccag	gcttgagggt	aagcgtgcaa	atggcaacat	ggaccccgct	660
ggtgccatcc	agtggagtgt	cattgatcga	tggccaacgc	accctggcct	cgtggaggct	720
ttcgcccggga	acattgagga	gcagctgaag	acatacccag	aggagaagcg	aaacgggtgtc	780
gttctcttgt	tctcagccca	cagtctgccc	atgagtgttg	tcaacagagg	cgacccatat	840
cctgctgaag	ttgctgcaac	tgtgcatgct	gtcatgcaaa	gattgaattt	cagcaatcct	900
taccgactgt	gctggcagtc	ccaagtggga	ccgtcagctt	ggcttggagc	ccaaactagc	960
gatacggctg	aaaactatgt	caaacgtgga	cagaccgata	ttattctagt	tcccattgcc	1020
ttcaccagcg	accatattga	gactctgtac	gagttggatc	tggaaagtga	aaaggaagca	1080
aactccccgg	gagtcaagag	agccgagagt	ttgaatggta	accccathtt	cattcaggca	1140
ttagcagaca	ttgcccga	gcacctccgt	aaggagagag	agtgtcact	acagatgact	1200
ctgcgctgtc	aaggctgtaa	gagcgaacgg	tgcctggaac	agaagaaatt	ctttgctggc	1260
gaccgatttt	cttctcttgt	agtttag				1287

<210> 110

<211> 428

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420
Protein sequence

<400> 110

Met	Ala	Leu	Arg	Arg	Pro	Leu	Thr	Leu	Pro	Arg	His	Ile	Leu	Asn	Gly
1				5					10					15	

Ala Cys Leu Gly Leu Arg Pro Ala Val Ser Arg Ala Ala Leu Ala Tyr
 20 25 30
 Gly Gln Glu Gln Arg Lys Gly Leu Ala Thr Ala Val Pro Pro Val Thr
 35 40 45
 Gln Asn Ala Ala Gly Ser Lys Gly Pro Thr Ala Met Val Phe Leu Asn
 50 55 60
 Met Gly Gly Pro Ser Lys Ile Asp Glu Val Glu Asp Phe Leu Ser Arg
 65 70 75 80
 Leu Phe Ala Asp Gly Asp Leu Ile Pro Leu Gly Arg Leu Gln Ser Tyr
 85 90 95
 Leu Gly Pro Leu Ile Ala Lys Arg Arg Thr Pro Lys Ile Gln Arg Gln
 100 105 110
 Tyr Ser Asp Ile Gly Gly Gly Ser Pro Ile Arg Lys Trp Ser Glu Tyr
 115 120 125
 Gln Cys Glu Glu Met Cys Arg Leu Leu Asp Lys Ile Asn Pro Glu Thr
 130 135 140
 Ala Pro His Lys Pro Tyr Val Ala Phe Arg Tyr Ala Asp Pro Leu Thr
 145 150 155 160
 Glu Glu Met Tyr Thr Lys Leu Leu Glu Asp Gly Phe Gly Asn Gly Lys
 165 170 175
 Gly Gly Arg Ala Val Ala Phe Thr Gln Tyr Pro Gln Tyr Ser Cys Ser
 180 185 190
 Thr Thr Gly Ser Ser Leu Asn Glu Leu Trp Lys Trp Arg Thr Arg Leu
 195 200 205
 Glu Gly Lys Arg Ala Asn Gly Asn Met Asp Pro Ala Gly Ala Ile Gln
 210 215 220
 Trp Ser Val Ile Asp Arg Trp Pro Thr His Pro Gly Leu Val Glu Ala
 225 230 235 240
 Phe Ala Arg Asn Ile Glu Glu Gln Leu Lys Thr Tyr Pro Glu Glu Lys
 245 250 255
 Arg Asn Gly Val Val Leu Leu Phe Ser Ala His Ser Leu Pro Met Ser
 260 265 270
 Val Val Asn Arg Gly Asp Pro Tyr Pro Ala Glu Val Ala Ala Thr Val
 275 280 285
 His Ala Val Met Gln Arg Leu Asn Phe Ser Asn Pro Tyr Arg Leu Cys
 290 295 300
 Trp Gln Ser Gln Val Gly Pro Ser Ala Trp Leu Gly Ala Gln Thr Ser
 305 310 315 320
 Asp Thr Val Glu Asn Tyr Val Lys Arg Gly Gln Thr Asp Ile Ile Leu
 325 330 335

Val Pro Ile Ala Phe Thr Ser Asp His Ile Glu Thr Leu Tyr Glu Leu
 340 345 350

Asp Leu Glu Val Ile Lys Glu Ala Asn Ser Pro Gly Val Lys Arg Ala
 355 360 365

Glu Ser Leu Asn Gly Asn Pro Ile Phe Ile Gln Ala Leu Ala Asp Ile
 370 375 380

Ala Gln Glu His Leu Arg Lys Gly Glu Lys Cys Ser Leu Gln Met Thr
 385 390 395 400

Leu Arg Cys Gln Gly Cys Lys Ser Glu Arg Cys Leu Glu Gln Lys Lys
 405 410 415

Phe Phe Ala Gly Asp Arg Phe Ser Ser Leu Val Val
 420 425

<210> 111

<211> 2865

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 111

ccttgatcga	atcccaagcc	tgtagcctgg	cagaacagag	caaagcaaac	tggcatctcc	60
tgctgaagcc	taaggctact	agacaaagga	acggcagaac	cgcatagaacg	aggagcataa	120
acaaggcggg	atcgtctttc	aacacgcggg	cggtgagctt	atcagcgccg	attgcgggggt	180
ggtgcagcaa	atcaagtcag	tcgccacttt	cggcgacat	gacaaagcgc	aagattgggt	240
ttactaaacc	gcctactttt	tttttatcaa	agagacttgg	gtttgtcagc	ttttctttat	300
cttctgaaag	agcgctttct	tggtcaagct	gttcaccaa	tccccatcac	tactgttccc	360
tttgtcgtaa	ttttcgctgc	attgcatcta	caacaaagaa	aacgggctcg	acgaaccctg	420
cgagatccat	acttcctggg	gtggcggtct	tcttagtcct	tatcgcatag	cggggtgctc	480
gaccagaagt	ccctgccacg	atgagtgcga	tcctttctgc	agacgatttg	aacgatttca	540
tttctcccg	ggttgcttgc	atcaagcccg	ttgagagtct	accacaaaaa	gaatcccagt	600
cggaggtatc	tttctgtct	taccagtcac	ctgttgatat	cagccaatag	gctaacgctc	660
atttccaatt	caatagaatc	cctatgaggt	gacaaaggaa	gacaaagttc	aaccggaaaa	720
ccttcccccg	gtcagatttt	cattgactga	ttgccttgca	tgctccggat	gtgtcacgctc	780
tgcggaagca	gtgttgatat	ccttgcaatc	acatacggag	gttctcaata	ctcttgattc	840
gtaccccgaa	ttgccgcttg	gttctacaag	ctaccaaaga	ggcacacaaa	aagttggatc	900
agcagacagc	gatggtcgca	tctttgttgc	tagcgtcagc	cctcaagtca	gggcgagctt	960
ggcagccaca	tacggaatca	ccgagcggga	ggcgaaatat	atgattgacc	aatttcttat	1020
gggcoctcac	ggtctcagag	ctggtggaaa	acatggcaat	gggtttacat	gggttgtgga	1080
cacgaacggt	atgcgtgaag	cagtgttggc	tctgacagcg	gacgaggtca	cgagctcttt	1140
attatcaact	ggatcgggca	gccttcccaa	gagtccaatt	ctttcgtccg	cttgccccgg	1200
ctggatatgt	tatgctgaaa	aaacacaccc	ttttatcctt	ccgcatttat	ctcgccctcaa	1260
gtctctcag	gcgttgagcg	gcacatttct	gaagtacgtg	ctaagcaagg	cacttgggggt	1320
ccgccttct	cagatatggc	atttagctat	catgccatgc	ttcgacaaga	agctggaagc	1380
tagccgggaa	gagctgacag	acattgcatg	ggcttcaacc	ttcaccagct	cacagacaac	1440
acccgtccgc	gacgttgact	gtgtcataac	caccgctgag	ctactaactt	tagccactgc	1500
tagggggctt	tctctaccca	atttgccgct	caaaccattg	cccgcgtcat	gtttaactcc	1560
atttccagat	caagccctag	aatcattttt	gttctctaag	agctcgtcgg	gccaaacagt	1620
cgaatcaggg	acatctggag	gctatcttca	tcacgtcctc	caaattcttc	aagccagaaa	1680
ccccggcagc	aagattgtca	cccagcgtgg	gcgcaacgcc	gatgttgtgg	aatatgtgct	1740
catgtcgtct	ggggatgagc	ctctttttag	ggcggtcgg	tattatgggt	tcaggaatat	1800
acaaaatctc	gtcagaaaac	ttaaaccgcg	acgcgtgtca	agactgccag	gcgccaagcc	1860
gcaagcgggtc	tcttcaagtg	caaatcgacg	acagcccatg	tcaaggaacg	cagctccggc	1920

tggaacaggc	gctgattatg	catatgttga	agtcattggct	tgtcctggcg	gctgtaccaa	1980
tggtggtggg	caaataagga	ttgaagatgc	ccgggaggct	gttccgaacg	cactaaaaga	2040
gacatcgact	gaaactcctg	tggctgcacc	gaaaccacg	ccgcatgagc	agcgtgcctg	2100
gctagcccgg	gtagatgaag	cgtactactc	tgcggactcg	gatagcgagg	gatctgtcac	2160
gacggagccg	gtttctgtcc	tgtcaaggga	taaccagatt	catgagtttt	tgaactattg	2220
gtcagagaag	ggtgatatac	ccctttcccg	gctcgcgtac	acgtcctatc	gcgaagtggg	2280
gagcgacgtg	ggtaagacga	agaatgcgcc	caacgaaact	gctcgtgttg	tggaattggc	2340
aggaaagatc	ggaggtgggt	ggtgatatcg	cactcgtgtg	ctggaaaaca	ttgcatatat	2400
ccattatacc	cttcaatttg	ttgtggatga	gaacgctcct	tgcactactg	gttggttgca	2460
tgctagtacg	catttggaga	gataccctt	tattatagat	ttctcatttg	ttgggcattt	2520
gagaggattt	ataagtcag	agattgctac	aggaagcccc	atagacgtat	agagatcagg	2580
gtagagcatg	ccaccttagc	ttttacacta	ctccgtacgg	tcatgatcaa	actcttgaat	2640
ttaatatattc	gattgctggac	aatcaaagca	atgtatggag	taaacatgtg	gtagagcagg	2700
tacctgaggc	ataacgtgct	agtccagaat	aggctagctc	catcaaacc	cgaatcttcc	2760
atcgggatga	caaagcagcc	tagagcattt	ggcagaaaaa	gtgctctacc	ccaagtctga	2820
attctctcca	acaactcgcc	ttcaatcacc	cacgccccag	tttat		2865

<210> 112

<211> 1865

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359
 Genomic sequence containing the coding region

<400> 112

atgagtgcaa	tcctttctgc	agacgatttg	aacgatttca	tttctcccg	ggttgcttgc	60
atcaagcccg	ttgagagtct	accacaaaaa	gaatcccagt	cggaggtatc	tttctgtct	120
taccagtcac	ctgttgatat	cagccaatag	gctaacgctc	atttccaatt	caatagaatc	180
cctatgaggt	gacaaaggaa	gacaaagttc	aaccggaaaa	ccttcccccg	gctcagattt	240
cattgactga	ttgccttgca	tgtctcggat	gtgtcacgctc	tgcggaagca	gtgttgatat	300
ccttgcaatc	acatacggag	gttctcaata	ctcttgattc	gtaccccgaa	ttgccgcttg	360
gttctacaag	ctaccaaaaga	ggcacacaaa	aagttggatc	agcagacagc	gatggtcgca	420
tctttgttgc	tagcgtcagc	cctcaagtca	ggcgagcgtt	ggcagccaca	tacggaatca	480
ccgagcggga	ggcgaaatat	atgattgacc	aatttcttat	gggccctcac	ggtctcagag	540
ctgggtggaaa	acatggcaat	gggtttacat	gggttgtgga	cacgaacgtt	atgcgtgaag	600
cagtggttggc	tctgacagcg	gacgaggtca	cgagctcttt	attatcaact	ggatcgggca	660
gccttcccaa	gagtccaatt	ctttcgtccg	cttgcccccg	ctggatatgt	tatgctgaaa	720
aaacacaccc	ttttatcctt	ccgcatttat	ctcgcctcaa	gtctcctcag	gcgttgagcg	780
gcacatttct	gaagtcagtg	ctaagcaagg	caattggggg	cccgccttct	cagatatggc	840
atttagctat	catgccatgc	ttcgacaaga	agctggaagc	tagccgggaa	gagctgacag	900
acattgcatg	ggcttcaacc	ttcaccagct	cacagacaac	acccgtccgc	gacgttgact	960
gtgtcataac	caccgtgag	ctactaactt	tagccactgc	taggggggctt	tctctaccca	1020
atttgccgct	caaaccattg	ccgcgctcat	gttttaactcc	atttccagat	caagccctag	1080
aatcattttt	gttctctaag	agctcgtcgg	gccaaacagt	cgaatcaggg	acatctggag	1140
gctatcttca	tcacgtcttc	caaactcttc	aagccagaaa	ccccggcagc	aagattgtca	1200
cccagcgtgg	gcgcaacgcc	gatgttgtgg	aatatgtgct	catgtcgtct	ggggatgagc	1260
ctcttttttag	ggcggtcgg	tattatggct	tcaggaatat	acaaaatctc	gtcagaaaac	1320
ttaaaccggc	acgcgtgtca	agactgccag	gcgccaagcc	gcaagcggtc	tcttcaagtg	1380
caaatcgacg	acagcccatg	tcaaggaacg	cagctccggc	tggaacaggc	gctgattatg	1440
catatgttga	agtcattggct	tgtcctggcg	gctgtacca	tggtggtggg	caaataagga	1500
ttgaagatgc	ccgggaggct	gttccgaacg	cactaaaaga	gacatcgact	gaaactcctg	1560
tggctgcacc	gaaaccacg	ccgcatgagc	agcgtgcctg	gctagcccgg	gtagatgaag	1620
cgtactactc	tgcggactcg	gatagcgagg	gatctgtcac	gacggagccg	gtttctgtcc	1680
tgtcaaggga	taaccagatt	catgagtttt	tgaactattg	gtcagagaag	gttgatatac	1740
ccctttcccg	gctcgcgtac	acgtcctatc	gcgaagtggg	gagcgacgtg	ggtaagacga	1800
agaatgcgcc	caacgaaact	gctcgtgttg	tggaattggc	aggaaagatc	ggaggtgggt	1860
ggtga						1865

<210> 113
 <211> 1725
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359
 Coding region without introns

```

<400> 113
atgagtgc aa tcttttctgc agacgatttg aacgatttca tttctcccgg ggttgcttgc      60
atcaagcccg ttgagagtct accacaaaaa gaatcccagt cggagaatcc ctatgagggtg      120
acaaaggaag acaaagtcca accggaaaac cttcccccg ctcagatttc attgactgat      180
tgccttgcat gctccggatg tgtcacgtct gcggaagcag tgttgatata cttgcaatca      240
catacggagg ttctcaatac tcttgattcc gatggctgca tctttgttgc tagcgctcagc      300
cctcaagtca gggcgagcct ggagccaca tacggaatca ccgagcggga ggcgaaatat      360
atgattgacc aatttcttat gggccctcac ggtctcagag ctggtggaaa acatggcaat      420
gggtttacat gggtgtgga cacgaacggt atgcgtgaag cagtgttggc tctgacagcg      480
gacgaggtca cgagctcttt attatcaact ggatcgggca gccttcccaa gagtccaatt      540
ctttcgtccg cttgccccgg ctggatatgt tatgctgaaa aaacacaccc ttttatcctt      600
ccgcatttat ctgcctcaa gtctcctcag gcgttgagcg gcacatttct gaagtcagtg      660
ctaagcaagg cacttggggg cccgccttct cagatatggc atttagctat catgccatgc      720
ttcgacaaga agctggaagc tagccgggaa gagctgacag acattgcatg ggcttcaacc      780
ttcaccaggt cacagacaac acccgctccg gacgttgact gtgtcataac cacccgtag      840
ctactaactt tagccactgc tagggggcct tctctacca atttgccgct caaaccattg      900
cccgcgctcat gtttaactcc atttccagat caagccctag aatcattttt gttctctaag      960
agctcgctcg gccaaacagt cgaatcaggg acatctggag gctatcttca tcacgtcctc     1020
caaatcttcc aagccagaaa ccccggcagc aagattgtca cccagcgtgg gcgcaacgcc     1080
gatgttgttg aatatgtgct catgtcgtct ggggatgagc ctcttttttag ggcggtcctg     1140
tattatggct tcaggaatat acaaaatctc gtcagaaaac ttaaaccgcg acgctgtgca     1200
agactgccag gcgccaagcc gcaagcgggc tcttcaagtg caaatcgacg acagcccatg     1260
tcaaggaacg cagctccggc tggaacaggg gctgattatg catatgttga agtcatggct     1320
tgtcctggcg gctgtacca tgggtgggtgg caaataagga ttgaagatgc ccgggagggt     1380
gttccgaacg cactaaaaga gacatcgact gaaactcctg tggctgcacc gaaaccacg     1440
ccgcatgagc agcgtgcctg gctagcccg gtagatgaag cgtactactc tgcggactcg     1500
gatagcgagg gatctgtcac gacggagccg gtttctgtcc tgtcaaggga taaccagatt     1560
catgagtttt tgaactattg gtcagagaag gttgatatac ccctttcccg gctcgcgtac     1620
acgtcctatc gcgaagtgga gagcgacgtg ggtaagacga agaatgcgcc caacgaaact     1680
gctcgtgttg tggaattggc aggaaagatc ggaggtggtt ggtga                        1725

```

<210> 114
 <211> 574
 <212> PRT
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359
 Protein sequence

<400> 114

```

Met Ser Ala Ile Leu Ser Ala Asp Asp Leu Asn Asp Phe Ile Ser Pro
1           5           10           15

Gly Val Ala Cys Ile Lys Pro Val Glu Ser Leu Pro Gln Lys Glu Ser
20          25          30

Gln Ser Glu Asn Pro Tyr Glu Val Thr Lys Glu Asp Lys Val Gln Pro
35          40          45

```

Glu Asn Leu Pro Pro Ala Gln Ile Ser Leu Thr Asp Cys Leu Ala Cys
 50 55 60
 Ser Gly Cys Val Thr Ser Ala Glu Ala Val Leu Ile Ser Leu Gln Ser
 65 70 75 80
 His Thr Glu Val Leu Asn Thr Leu Asp Ser Asp Gly Arg Ile Phe Val
 85 90 95
 Ala Ser Val Ser Pro Gln Val Arg Ala Ser Leu Ala Ala Thr Tyr Gly
 100 105 110
 Ile Thr Glu Arg Glu Ala Lys Tyr Met Ile Asp Gln Phe Leu Met Gly
 115 120 125
 Pro His Gly Leu Arg Ala Gly Gly Lys His Gly Asn Gly Phe Thr Trp
 130 135 140
 Val Val Asp Thr Asn Val Met Arg Glu Ala Val Leu Ala Leu Thr Ala
 145 150 155 160
 Asp Glu Val Thr Ser Ser Leu Leu Ser Thr Gly Ser Gly Ser Leu Pro
 165 170 175
 Lys Ser Pro Ile Leu Ser Ser Ala Cys Pro Gly Trp Ile Cys Tyr Ala
 180 185 190
 Glu Lys Thr His Pro Phe Ile Leu Pro His Leu Ser Arg Leu Lys Ser
 195 200 205
 Pro Gln Ala Leu Ser Gly Thr Phe Leu Lys Ser Val Leu Ser Lys Ala
 210 215 220
 Leu Gly Val Pro Pro Ser Gln Ile Trp His Leu Ala Ile Met Pro Cys
 225 230 235 240
 Phe Asp Lys Lys Leu Glu Ala Ser Arg Glu Glu Leu Thr Asp Ile Ala
 245 250 255
 Trp Ala Ser Thr Phe Thr Gln Ser Gln Thr Thr Pro Val Arg Asp Val
 260 265 270
 Asp Cys Val Ile Thr Thr Arg Glu Leu Leu Thr Leu Ala Thr Ala Arg
 275 280 285
 Gly Leu Ser Leu Pro Asn Leu Pro Leu Lys Pro Leu Pro Ala Ser Cys
 290 295 300
 Leu Thr Pro Phe Pro Asp Gln Ala Leu Glu Ser Phe Leu Phe Ser Lys
 305 310 315 320
 Ser Ser Ser Gly Gln Thr Val Glu Ser Gly Thr Ser Gly Gly Tyr Leu
 325 330 335
 His His Val Leu Gln Ile Phe Gln Ala Arg Asn Pro Gly Ser Lys Ile
 340 345 350
 Val Thr Gln Arg Gly Arg Asn Ala Asp Val Val Glu Tyr Val Leu Met
 355 360 365

Ser Ser Gly Asp Glu Pro Leu Phe Arg Ala Ala Arg Tyr Tyr Gly Phe
 370 375 380
 Arg Asn Ile Gln Asn Leu Val Arg Lys Leu Lys Pro Ala Arg Val Ser
 385 390 395 400
 Arg Leu Pro Gly Ala Lys Pro Gln Ala Val Ser Ser Ser Ala Asn Arg
 405 410 415
 Arg Gln Pro Met Ser Arg Asn Ala Ala Pro Ala Gly Thr Gly Ala Asp
 420 425 430
 Tyr Ala Tyr Val Glu Val Met Ala Cys Pro Gly Gly Cys Thr Asn Gly
 435 440 445
 Gly Gly Gln Ile Arg Ile Glu Asp Ala Arg Glu Ala Val Pro Asn Ala
 450 455 460
 Leu Lys Glu Thr Ser Thr Glu Thr Pro Val Ala Ala Pro Lys Pro Thr
 465 470 475 480
 Pro His Glu Gln Arg Ala Trp Leu Ala Arg Val Asp Glu Ala Tyr Tyr
 485 490 495
 Ser Ala Asp Ser Asp Ser Glu Gly Ser Val Thr Thr Glu Pro Val Ser
 500 505 510
 Val Leu Ser Arg Asp Asn Gln Ile His Glu Phe Leu Asn Tyr Trp Ser
 515 520 525
 Glu Lys Val Asp Ile Pro Leu Ser Arg Leu Ala Tyr Thr Ser Tyr Arg
 530 535 540
 Glu Val Glu Ser Asp Val Gly Lys Thr Lys Asn Ala Pro Asn Glu Thr
 545 550 555 560
 Ala Arg Val Val Glu Leu Ala Gly Lys Ile Gly Gly Gly Trp
 565 570

<210> 115

<211> 1510

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 115

taagagttgc	aggtatgagc	ctggtaaate	aagtcagtc	cggatagcac	aacagaacct	60
cattttgtcc	tgaaagaatg	aacaaaaagg	ccaactcaga	ctctttgcaa	atgcaaggaa	120
gaggtaatga	gaatgttttg	ggagaagctt	aaatgtagct	ttgccggaac	ggagaattga	180
gtaaagccgg	tcatgaggcg	ccaagacccc	agcgaaaaag	cagccctagg	ccgcacgcaa	240
ccccgttcgg	cgagttgcta	ctggctgtta	agcgagactc	ttgtgggcca	agaccgcaac	300
acccgaaatt	cgcgatccag	tagcccagag	cgacttggtg	gcgtttcgga	cgactttgac	360
aatccccgact	cttcgacaac	aaattcccat	caccgccctc	ccggagtctg	tcgaccgtga	420
gtttgaaacc	tacgccctat	cgaatttctg	gactgtcaact	gaagaatccg	tttttgtcgt	480
tttttttagga	agccttcgcc	atggccgata	tcgatgtcaa	ggttgctcaa	tggaagcttg	540
ttgaggttgg	ccgtgtttgt	ctgatccgca	gcggtcctta	caccggcaag	cttgctgcca	600
ttgtcgagat	catcgaccac	aagcgtgtac	gtttttcaac	ggagaaattc	tgagcgcagg	660

acggaaagat	catgggtcggg	tgtgatattg	acaaagaggc	gcgatcatag	gtcctgggtg	720
acggtccttc	caccgaggag	aacaagatcg	ttccccgtca	cgctcttcct	ctcgctcacg	780
ccactctcac	ccccttcgtc	attcccaaac	tcccccgcg	tgccggcact	ggccccgtca	840
agaagctctg	ggagaagaac	gagatcgatg	gaaagtgggc	taagagcacc	attgctcaga	900
agactgagcg	cgctgagcgg	aggaagaacc	ttaccgactt	cgagcgcttc	aaggtcctca	960
gactcaagaa	gcaggtacgt	tcagtttgcg	aaactatggg	agaattgtga	tggcacattg	1020
gagggcattc	ttggcaactc	tgcactcgct	tttcgcgaga	gggaagagga	gcaattactt	1080
gtattatgat	ttgcgactgg	ttactgacat	ctggtgattt	aacaggctcg	ctacgaggtc	1140
cagaaggctc	acgccaaggt	cagggctgct	gctcctaagt	catagatgtt	ttcatgaggc	1200
tcggtgcata	gtatgaaggg	gtaccttggg	acggttttac	atggctgagg	gttttattct	1260
atttcagcaa	aaattaagct	gtatccacta	caatgacagc	caaaaaatga	ttcaaacctt	1320
tgatatacctg	acacgggtca	tcctgctatg	tcatcagatt	cgcgaccccg	attagtactt	1380
ggctctggtt	tatagccgtc	tccttagaca	ttaattggga	attaaacatt	ttagactcaa	1440
gatcacggaa	tatgtaagaa	agtatcggtt	tgtacattac	tgagttggat	tggctcggtt	1500
tgactcgtat						1510

<210> 116

<211> 685

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619
Genomic sequence containing the coding region

<400> 116

atggccgata	tcgatgtcaa	ggttgctcaa	tggaagcttg	ttgaggttgg	ccgtgttgtg	60
ctgatccgca	gcggtcctta	caccggcaag	cttgctgcca	ttgtcgagat	catcgaccac	120
aagcgtgtac	gtttttcaac	ggagaaattc	tgagcgcagg	acggaaagat	catgggtcggg	180
tgtgatattg	acaaagaggc	gcgatcatag	gtcctgggtg	acggtccttc	caccgaggag	240
aacaagatcg	ttccccgtca	cgctcttcct	ctcgctcacg	ccactctcac	ccccttcgtc	300
attcccaaac	tcccccgcg	tgccggcact	ggccccgtca	agaagctctg	ggagaagaac	360
gagatcgatg	gaaagtgggc	taagagcacc	attgctcaga	agactgagcg	cgctgagcgg	420
aggaagaacc	ttaccgactt	cgagcgcttc	aaggtcctca	gactcaagaa	gcaggtacgt	480
tcagtttgcg	aaactatggg	agaattgtga	tggcacattg	gagggcattc	ttggcaactc	540
tgcactcgct	tttcgcgaga	gggaagagga	gcaattactt	gtattatgat	ttgcgactgg	600
ttactgacat	ctggtgattt	aacaggctcg	ctacgaggtc	cagaaggctc	acgccaaggt	660
cagggctgct	gctcctaagt	catag				685

<210> 117

<211> 465

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619
Coding region without introns

<400> 117

atggccgata	tcgatgtcaa	ggttgctcaa	tggaagcttg	ttgaggttgg	ccgtgttgtg	60
ctgatccgca	gcggtcctta	caccggcaag	cttgctgcca	ttgtcgagat	catcgaccac	120
aagcgtgtcc	tggttgacgg	tccttcacc	gaggagaaca	agatcgttcc	ccgtcacgct	180
cttctctctg	ctcagccac	tctcaccccc	ttcgtcattc	ccaaactccc	ccgcgctgcc	240
ggcactggcc	ccgtcaagaa	gctctgggag	aagaacgaga	tcgatggaaa	gtgggctaag	300
agcaccattg	ctcagaagac	tgagcgcgct	gagcggagga	agaaccttac	cgacttcgag	360
cgcttcaagg	tcctcagact	caagaagcag	gctcgtacg	aggtccagaa	ggctcacgcc	420
aaggtcaggg	ctgctgctcc	taagtcatag	atgttttcat	gagggc		465

<210> 118

<211> 149
 <212> PRT
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619
 Protein sequence

<400> 118

```

Met Ala Asp Ile Asp Val Lys Val Ala Gln Trp Lys Leu Val Glu Val
 1             5             10             15
Gly Arg Val Val Leu Ile Arg Ser Gly Pro Tyr Thr Gly Lys Leu Ala
          20             25             30
Ala Ile Val Glu Ile Ile Asp His Lys Arg Val Leu Val Asp Gly Pro
          35             40             45
Ser Thr Glu Glu Asn Lys Ile Val Pro Arg His Ala Leu Pro Leu Ala
          50             55             60
His Ala Thr Leu Thr Pro Phe Val Ile Pro Lys Leu Pro Arg Ala Ala
          65             70             75             80
Gly Thr Gly Pro Val Lys Lys Leu Trp Glu Lys Asn Glu Ile Asp Gly
          85             90             95
Lys Trp Ala Lys Ser Thr Ile Ala Gln Lys Thr Glu Arg Ala Glu Arg
          100            105            110
Arg Lys Asn Leu Thr Asp Phe Glu Arg Phe Lys Val Leu Arg Leu Lys
          115            120            125
Lys Gln Ala Arg Tyr Glu Val Gln Lys Ala His Ala Lys Val Arg Ala
          130            135            140

Ala Ala Pro Lys Ser
145

```

<210> 119
 <211> 1942
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221
 Genomic sequence containing 3' and 5'-ends and the coding region

```

<400> 119
tacacccagc acacctaccc tagccacaga tttcttggac cacgggaacc cgaacaaaga      60
gtctctggcc gaactctggt ctaatttctt agagcaggag tcacaggcca gtgggaatcc      120
agaatcgccg aaaccatgaa gagtttcaaa aggtggctct gttctgagcc gtatagaaaa      180
ctagcatctt ctctaagata cgggtggttc acatttatat atgcttgccg actggctttg      240
gtctcctctt cttttccatt ctgacttgct ttcgtagtaa taacactgat atcaccgcg      300
tgtttgcgac ttttgcacaa aaccagcttc cccaccgctt tctttctgcc accatagcgg      360
gggacctcgt tattgagcgg acaagtcgtc gttggctttt tctgcacggt tggcctatgc      420
ttcgtttatt cagctctggt acagctggga agttgactga tacactctcc tctctgattt      480
cttggtactc cagattgaca atgactaccg gggctggtac gatctctcat tccaacacct      540
atcatcgtat tcctcgccgt taactgacca atccaccagt gcaaagggtc cgtccagtgg      600
tggtatcggg tccctctggg actgggaagt cgaccttgct caagagactc ttcgctgaat      660

```

accccgatac	tttcgattta	tccgtgtctc	gtacgtctaa	ccccttgcca	accctcattg	720
actatgcctg	cgaattgttt	cttttggttg	aattgcgctg	aacggtgttt	gttatattta	780
gataccactc	gagctccccg	tcccggggaa	gaaaatggac	gtgagtatta	cttcacaact	840
aaagaagatt	tcctggatct	tgtgagcaag	aatgccttta	tcgagcatgc	gcagtttggt	900
ggcaattact	acggtactac	tgtgcaggca	gtgaaggatg	ttgcgcagaa	gggcaagatc	960
tgcgttctcg	acattgagat	gaggtaataa	tagtcctgca	acgtgaactg	atatgaccgg	1020
agaagcagag	gaaatccatc	atcaaagtga	ttgtagttca	acccaaacaa	cagctgacga	1080
ctgaattgca	atagggcggtg	aaacaagtca	agcgcaccga	tcttgatgct	cgattcttat	1140
tttttagcacc	cccgtccctt	gaagaactag	agaaaagact	gcgtgggaga	gcaaccgaga	1200
ctgaggagag	cttgacggta	tggctgtcct	ccacattcct	tcacttcccc	aactcgccag	1260
actgtccccg	tggaattcta	actttgcgtc	agaaacgcct	tgcccaagct	aaaaatgaat	1320
tggaatatgc	ggcgcagcct	ggctctcatg	ataagattgt	cgtgaacgat	gacctggaga	1380
aggcttataa	ggaactgcgg	gattggattg	tcgacgggtg	taactttgga	gcgcgtcaat	1440
gatttattgg	gcatgtctcg	gcgtgtttta	tttatcagcg	ctgctgtata	ctttagcgcc	1500
cgtagatact	gtcggttgcg	atactgaaaa	caatgcatca	tctgccttgg	taacttcggt	1560
ccacagaaac	ccataatcaa	ggaggtcctt	tcgtcgtcga	cgaacataag	agagattaat	1620
tacatgaaca	tcaagactat	gctaacaatt	cgaatgttgg	tctcttttct	gtctggagac	1680
gacaaatcta	ggaaagggtg	tagactcagt	cactctcttg	aacggagagg	agaaaattaa	1740
gcaaaactaa	aaaagagaac	aaagtctgat	gagcaatatg	agggctgaaa	aggatatctg	1800
taaagaggct	gctagaataa	aatggaagat	gccgattgag	aaggcaatgg	aggaagagaa	1860
gggggtcattt	atcgcagttt	ggcgtgggac	cagaaatgac	tgcagtatgt	ttatggacca	1920
tgccagccgg	agctattgga	ct				1942

<210> 120

<211> 943

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221
Genomic sequence containing the coding region

<400> 120

atgactaccg	gggctggtac	gatctctcat	tccaacacct	atcatcgtat	tcctcgccgt	60
taactgacca	atccaccagt	gcaaagggtc	cgtccagtg	tggtatcggg	tccctctggg	120
actgggaagt	cgaccttgct	caagagactc	ttcgctgaat	accccgatac	tttcgattta	180
tccgtgtctc	gtacgtctaa	ccccttgcca	accctcattg	actatgcctg	cgaattgttt	240
cttttggtgg	aattgcgctg	aacggtgttt	gttatattta	gataccactc	gagctccccg	300
tcccggggaa	gaaaatggac	gtgagtatta	cttcacaact	aaagaagatt	tcctggatct	360
tgtgagcaag	aatgccttta	tcgagcatgc	gcagtttggt	ggcaattact	acggtactac	420
tgtgcaggca	gtgaaggatg	ttgcgcagaa	gggcaagatc	tgcgttctcg	acattgagat	480
ggaggttaata	atagtccctg	aacgtgaact	gatatgaccg	gagaagcaga	ggaaatccat	540
catcaaattg	attgtagtct	aacccaaaca	acagctgacg	actgaattgc	aatagggcgt	600
gaaacaagtc	aagcgcaccg	atcttgatgc	tcgattctta	tttttagcac	ccccgtccct	660
tgaagaacta	gagaaaagac	tgcgtgggag	agcaaccgag	actgaggaga	gcttgacggg	720
atggctgtcc	tccacattcc	ttcacttccc	caactcgcca	gactgtcccc	ctggaattct	780
aactttgcgt	cagaaacgcc	ttgcccgaag	taaaaatgaa	ttggaatatg	cggcgcagcc	840
tggctctcat	gataagattg	tcgtgaacga	tgacctggag	aaggcttata	aggaactgcg	900
ggattggatt	gtcgcaggtg	gtaacttttg	agcgcgtcaa	tga		943

<210> 121

<211> 603

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221
Coding region without introns

```

<400> 121
atgactaccg gggctgtgca aaggttccgt ccagtgggtg tatcgggtcc ctctgggact    60
gggaagtcga ccttgctcaa gagactcttc gctgaatacc ccgatacttt cgatttatcc    120
gtgtctcata ccaactcgagc tccccgtccc ggggaagaaa atggacgtga gtattacttc    180
acaactaaag aagatttcct ggatcttggt agcaagaatg cctttatcga gcatgcgag    240
tttgggtggca attactacgg tactactgtg caggcagtga aggatgttgc gcagaagggc    300
aagatctgcg ttctcgacat tgagatggag ggcgtgaaac aagtcaagcg caccgatctt    360
gatgctcgat tcttattttt agcaccctccg tcccttgaag aactagagaa aagactgcgt    420
gggagagcaa ccgagactga ggagagcttg acgaaacgcc ttgcccagc taaaaatgaa    480
ttggaatatg cggcgagacc tggctctcat gataagattg tcgtgaacga tgacctggag    540
aaggcttata aggaactgcg ggattggatt gtcgacggtg gtaactttgg agcgcgtcaa    600
tga                                                                    603

```

<210> 122

<211> 200

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221
Protein sequence

<400> 122

```

Met Thr Thr Gly Ala Val Gln Arg Phe Arg Pro Val Val Val Ser Gly
1          5          10          15

Pro Ser Gly Thr Gly Lys Ser Thr Leu Leu Lys Arg Leu Phe Ala Glu
          20          25          30

Tyr Pro Asp Thr Phe Asp Leu Ser Val Ser His Thr Thr Arg Ala Pro
          35          40          45

Arg Pro Gly Glu Glu Asn Gly Arg Glu Tyr Tyr Phe Thr Thr Lys Glu
          50          55          60

Asp Phe Leu Asp Leu Val Ser Lys Asn Ala Phe Ile Glu His Ala Gln
65          70          75          80

Phe Gly Gly Asn Tyr Tyr Gly Thr Thr Val Gln Ala Val Lys Asp Val
          85          90          95

Ala Gln Lys Gly Lys Ile Cys Val Leu Asp Ile Glu Met Glu Gly Val
          100         105         110

Lys Gln Val Lys Arg Thr Asp Leu Asp Ala Arg Phe Leu Phe Leu Ala
          115         120         125

Pro Pro Ser Leu Glu Glu Leu Glu Lys Arg Leu Arg Gly Arg Ala Thr
          130         135         140

Glu Thr Glu Glu Ser Leu Thr Lys Arg Leu Ala Gln Ala Lys Asn Glu
145          150         155         160

Leu Glu Tyr Ala Ala Gln Pro Gly Ser His Asp Lys Ile Val Val Asn
          165         170         175

Asp Asp Leu Glu Lys Ala Tyr Lys Glu Leu Arg Asp Trp Ile Val Asp
          180         185         190

```

Gly Gly Asn Phe Gly Ala Arg Gln
195 200

<210> 123

<211> 3108

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 123

aaaccaggcg	catatgttcc	gctgccgccc	tgcgcaggag	agggctgata	aggattgccca	60
tatccagacg	acgggggctg	ctgggatgct	gggggaggag	gcgagcgcat	catgggaacg	120
gtagatacat	gctgaggcac	aggatggtgg	agtggagggtg	actgcgcagg	cggtggtgcg	180
aaagactggc	ggtacatggt	gatttttttt	tcccttggtta	caataagtga	gaagctagtg	240
atgaacaaaa	gacttgcgac	tattctgtct	cgtcttcttg	tcttctacca	accgaagagg	300
ggggatggtg	gaaatcggac	agtttgagta	tgagtgatgt	tgaagtgtgt	ttatacgtgg	360
ctggactcgg	tctgatcgcc	ggagagctct	caccttttcc	gccacagggt	ccccaccata	420
gtggccacta	cacacacttg	tccgttctcc	aaaaccacag	ctgctcgac	tgaataatat	480
acacaagaag	tgcttacaac	atgttagaag	ccttcgaagt	cttgacaaca	tctgggggtg	540
tgctgtggtc	gaagtcgtat	gcgccggctc	gagcgcatgt	tgtcaacagc	ctaataacag	600
atgtcttcat	tgaggagaag	gttcgagcgc	agaatcaggc	agcgagcagt	gcagctccta	660
tctacaagaa	ggaaaagtat	actctgaaat	ggaagcaagt	aaaggatttc	aatctgatat	720
ttgtggtatg	ttcacgccgc	tcggtgattc	aatggcgcca	ctgaccgatt	ccataggctg	780
tatatcaatc	tctgtacat	cttggttgga	tcgacaaact	cttgataat	gtttcgacca	840
tattcatcga	cttatataag	gatgagctaa	ggagcacacg	ggctaggatt	attgagtacc	900
cattcgataa	gtacttcgac	cagcagggtgc	gagagcttga	ggacaatgct	ggggctccta	960
catcagaatc	tctcgtagta	gagatcaacg	agagaaagga	ccctcttgct	tcatcagata	1020
acggcgggcc	acctccgcca	cccgtgcctg	gtctgctgaa	aggatatctga	cgtcgataat	1080
ttttctctgc	tagtgatcat	attgctaact	acctccgaag	cgcaacgtcc	agttgcgcag	1140
ggcgtggcga	cctcggaacg	gggttcgccca	ccccaaaccc	cagatctttc	tcgatcgta	1200
acgcccattt	caggtcatct	attgaccgcg	aaaggagggg	ctgctggccg	cgcctctcgt	1260
cgcgcacgca	aagcggccaa	cgcgagcgct	accgctctct	ctggagatga	aagcattcgg	1320
aaggggaaaa	cattgaaaag	tggaaaaaag	atgcgcaagt	gggatgctga	tggctttgcg	1380
gatgaggacg	acggcaaggt	cctcgattac	tccgcccccg	cagatggtga	ggacgcaccg	1440
gctcctgtag	tcgaggctgt	tgcgcaggaa	tcctggggac	gccgaacagg	caagggccaa	1500
tttgtgctga	aagatctagg	ggatgaagtc	cattccattc	ttgagaatgc	tgatcatgaa	1560
aagacaaaag	cttcctcgtc	cacgggcttt	gttgggtctg	gagtcaacgc	acttggtgga	1620
ttcttccgta	atattgtcgg	cggcaaggtc	cttactgagg	ctgacttgga	gaaacccttg	1680
aaagccatgg	aagaccattt	gctgaagaag	aacgttgccg	gcgaagcggc	cgtccgtcta	1740
tgtcaaggcg	tccagcgcgga	attagttggc	aagaagacag	gcaactttca	aagtgttgat	1800
gcagactgc	gctccgcaat	ggagtccctc	ttgcgcaaaa	tattgacgcc	aacgtcatct	1860
ctcgatctac	tgcgtgagat	cgatgctggt	agatctccga	cgagcaaaag	acaggctcct	1920
cgcccatatg	tcatttccat	cgtgggcgtg	aacgggtgtg	ggaagtcgac	aaatctgggc	1980
aaaatttgtt	acttccttct	ccagaataac	tatcgtgttc	tgattgcagc	ctgtgacacc	2040
ttccgctctg	gagccgtgga	gcagttacga	gtccatgctc	gcaatttgaa	ggaacttagt	2100
acccgggaga	atgctggaga	ggttgaactc	tacgagaagg	gatatggaaa	ggatgcagcg	2160
aatgtagcga	aggatgcagt	ggagtacggt	gcggcgaaatc	atttcgacgt	tgtgttgatt	2220
gatactgccg	gtcgccgtca	taacgaccaa	cgccttatgt	cttcgctcga	gaagttcgcc	2280
aagttcgcca	aaccagataa	gatcttcatg	gtcgggtgaag	ctctggtcgg	tacggacagc	2340
gtgatgcagg	ctcgcaactt	caaccaagct	ttcggcactg	ggagaaacct	cgatgggttc	2400
atcatcagta	aatgtgatac	cgttggtgac	atggtaggta	cgcttgctcag	catggtgcat	2460
gctacaggca	ttcctattgt	ttttctgggt	gtaggccagc	actatggtga	tttgaggggc	2520
ctaagtgttc	cttgggctgt	caatctgctg	atgaagtgag	cgcgcagctt	ttgccttgta	2580
atagagaatt	atattatctc	gcttctgate	acgctgggtc	ttggatggcc	ttcttcaaaa	2640
ataagttact	gcgattgtac	atctcgcgct	tcgctaaaga	tagagaaacg	aaagatagac	2700
aaagaacggg	ggaaaaaatt	gacaaaaaga	atgacctacg	caggattcga	acctgcaatc	2760
tcttgatccg	tagtcaagcg	ccttaccatt	gggccagcag	gccttcttga	aggttttcac	2820

ccagaaatat	gctttatcag	gaatctggga	acatccgcat	aaactccaat	aataagcttg	2880
tgccgtgcat	tgttactacg	ctaaagtgc	tctctagtgt	ggctcttatg	caggagaaac	2940
catacaggat	attgtaacgg	tgaatgcatt	ttttctgcct	tgaggtatga	caccattttg	3000
ttttggaggt	ggactcgatc	acgagctcac	tatcccggcc	tcatgggagg	attatgacac	3060
ccttggttcc	tgaataacttg	gtcttggtcg	gaattacttc	aatgacac		3108

<210> 124

<211> 2059

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167
Genomic sequence containing the coding region

<400> 124

atgttagaag	ccttcgaagt	cttgacaaca	tctgggggtg	tgctgtggtc	gaagtcgtat	60
gcgcgggtcg	gagcgcattg	tgtcaacagc	ctaatacaacg	atgtcttcat	tgaggagaag	120
gttcgagcgc	agaatcaggc	agcgcagcag	gcagctccta	tctacaagaa	ggaaaagtat	180
actctgaaat	ggaagcaagt	aaaggatttc	aatctgatat	ttgtgggtatg	ttcacgccgc	240
tcgttgattc	aatggcgcca	ctgaccgatt	ccataggctg	tatatcaatc	tctgctacat	300
cttggtttga	tcgacaaact	cttgataat	gtttcgacca	tattcatcga	cttatataag	360
gatgagctaa	ggagcacacg	ggctaggatt	attgagtacc	cattcgataa	gtacttcgac	420
cagcaggtgc	gagagcttga	ggacaatgct	ggggctccta	catcagaatc	tctcgtagta	480
gagatcaacg	agagaaagga	ccctcttgct	tcatcagata	acggcggggc	acctccgcca	540
cccgtgcctg	gtctgctgaa	aggtatctga	cgctcgataat	ttttctctgc	tagtgatcat	600
attgctaact	acctccgaag	cgcaacgtcc	agttgcgcag	ggcgtggcga	cctcggacga	660
gggttcgcca	ccccaaacc	cagatctttc	tcgatcgtca	acgcccattt	cagggtcatct	720
attgaccgcg	aaaggagggc	ctgctggccg	cgctctcgt	cgcgacgcga	aagcggccaa	780
cgcgagcgct	accgcttctt	ctggagatga	aagcattcgg	aaggggaaaa	cattgaaaag	840
tggaaaaaag	atgcgcaagt	gggatgctga	tggctttgcg	gatgaggacg	acggcaaggt	900
cctcgattac	tccgcccccg	cagatggtga	ggacgcaccg	gctcctgtag	tcgaggctgt	960
tgcgcaggaa	tcctggggac	gccgaacagg	caagggccaa	tttgtgctga	aagatctagg	1020
ggatgaagtc	cattccattc	ttgagaatgc	tgatcatgaa	aagacaaagt	cttctcgtc	1080
cacgggcttt	gttgggtctg	gagtcaacgc	acttggtgga	ttcttccgta	atattgtcgg	1140
cggaaggctc	cttactgagg	ctgacttgga	gaaacccttg	aaagccatgg	aagaccattt	1200
gctgaagaag	aacgttgcgc	gcgaagcggc	cgctcgtcta	tgtcaaggcg	tccagcgcgga	1260
attagttggc	aagaagacag	gcaactttca	aagtgttgat	gcagcactgc	gctccgcaat	1320
ggagtccctg	ttgcgcaaaa	tattgacgcc	aacgtcatct	ctcgatctac	tgctgagat	1380
cgatgctgtt	agatctccga	cgagcaaagg	acaggctcct	cgcccatatg	tcatttccat	1440
cgtgggctgt	aacggtgttg	ggaagtgcac	aaatctgggc	aaaatttggt	acttccttct	1500
ccagaataac	tatcggttgc	tgattgcagc	ctgtgacacc	ttccgctctg	gagccgtgga	1560
gcagttacga	gtccatgctc	gcaatttgaa	ggaacttagt	acccgggaga	atgctggaga	1620
ggttgaaact	tacgagaagg	gatatggaaa	ggatgcagcg	aatgtagcga	aggatgcagt	1680
ggagtacggt	gcggcgaaatc	atttcgacgt	tgtgttgatt	gatactgccg	gtcggcgtca	1740
taacgaccaa	cgcttatatg	cttcgctcga	gaagttcgcc	aagttcgcca	aaccagataa	1800
gatcttcatg	gtcgtggaag	ctctggctcg	tacggacagc	gtgatgcagg	ctcgcaactt	1860
caaccaagct	ttcggcactg	ggagaaacct	cgatgggttc	atcatcagta	aatgtgatac	1920
cgttgggtgac	atggtaggta	cgcttgctcag	catggtgcat	gctacaggca	ttcctattgt	1980
ttttctgggt	gtaggccagc	actatggtga	tttgaggggc	ctaagtgttc	cttgggctgt	2040
caatctgctg	atgaagtga					2059

<210> 125

<211> 1884

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167

Coding region without introns

```

<400> 125
atgttagaag ccttcgaagt cttgacaaca tctgggggtgg tgctgtgggtc gaagtcgtat    60
ggcgcgggtcg gagcgcatgt tgtcaacagc ctaatcaacg atgtcttcat tgaggagaag    120
gttcgagcgc agaatcaggc agcgagcagt gcagctccta tctacaagaa ggaaaagtat    180
actctgaaat ggaagcaagt aaaggatttc aatctgatat ttgtgcttgg ttggatcgac    240
aaactcttgg ataatgtttc gaccatattc atcgacttat ataaggatga gctaaggagc    300
acacgggcta ggattattga gtacccattc gataagtact tcgaccagca ggtgcgagag    360
cttgaggaca atgctggggc tcctacatca gaatctctcg tagtagagat caacgagaga    420
aaggaccctc ttgtctcatc agataacggc ggccacctc cgccaccgt gcctgcctcg    480
gacgagggtt cgccacccca aaccccgat ctttctcgat cgtcaacgcc catttcaggt    540
catctattga ccgcgaaagg agggcctgct ggccgcgcct ctgctcgcg acgcaaagcg    600
gccaacgcga gcgctaccgc ttcttctgga gatgaaagca ttcggaaggg gaaaacattg    660
aaaagtggaa aaaagatgcg caagtgggat gctgatggct ttgcggatga ggacgacggc    720
aaggtcctcg attactccgc ccccgagat ggtgaggacg caccggctcc tgtagtcgag    780
gctgttgcg aggaatcctg gggacgccga acaggcaagg gccaatttgt gctgaaagat    840
ctaggggatg aagtccattc cattcttgag aatgctgac atgaaaagac aaagtcttcc    900
tcgtccacgg gctttgttgg gtctggagtc aacgcacttg gtggattctt ccgtaatat    960
gtcggcggca agtccttac tgaggctgac ttggagaaac ccttgaaagc catggaagac   1020
catttgctga agaagaacgt tgcgcgcgaa gcggccgtcc gtctatgtca aggcgtccag   1080
cgcaattag ttggcaagaa gacaggcaac tttaaagtg ttgatgcagc actgcgctcc   1140
gcaatggagt cctcgttgcg caaaatattg acgccaacgt catctctcga tctactgcgt   1200
gagatcgatg ctgttagatc tccgacgagc aaaggacagg ctctcgccc atatgtcatt   1260
tccatcgtag gcgtgaacgg tgttggaag tcgacaaatc tgggcaaaat ttgttacttc   1320
cttctccaga ataactatcg tgttctgatt gcagcctgtg acaccttccg ctctggagcc   1380
gtggagcagt tacgagtcca tgctcgcaat ttgaaggaaac ttagtaccgg ggagaatgct   1440
ggagaggttg aactctacga gaaggatat ggaaaggatg cagcgaatgt agcgaaggat   1500
gcagtggagt acggtgcggc gaatcatttc gacgttgtgt tgattgatac tgccggtcgc   1560
cgtcataacg accaacgcct tatgtcttcg ctcgagaagt tcgccaagtt cgccaaacca   1620
gataagatct tcatggtcgg tgaagctctg gtcggtacgg acagcgtgat gcaggctcgc   1680
aacttcaacc aagctttcgg cactgggaga aacctcgatg ggttcatcat cagtaaagt   1740
gataccgttg gtgacatggg aggtacgctt gtcagcatgg tgcattgctac aggcattcct   1800
attgtttttc tgggtgtagg ccagcactat ggtgatttga ggggcctaag tgttccttgg   1860
gctgtcaatc tgctgatgaa gtga

```

<210> 126

<211> 641

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167
Protein sequence

<400> 126

```

Met Leu Glu Ala Phe Glu Val Leu Thr Thr Ser Gly Val Val Leu Trp
1          5          10          15

```

```

Ser Lys Ser Tyr Ala Pro Val Gly Ala His Val Val Asn Ser Leu Ile
          20          25          30

```

```

Asn Asp Val Phe Ile Glu Glu Lys Val Arg Ala Gln Asn Gln Ala Ala
          35          40          45

```

```

Ser Ser Ala Ala Pro Ile Tyr Lys Lys Glu Lys Tyr Thr Leu Lys Trp
          50          55          60

```

```

Lys Gln Val Lys Asp Phe Asn Leu Ile Phe Val Ala Val Tyr Gln Ser

```

65	70	75	80
Leu Leu His Leu Gly Trp Ile Asp Lys Leu Leu Asp Asn Val Ser Thr	85	90	95
Ile Phe Ile Asp Leu Tyr Lys Asp Glu Leu Arg Ser Thr Arg Ala Arg	100	105	110
Ile Ile Glu Tyr Pro Phe Asp Lys Tyr Phe Asp Gln Gln Val Arg Glu	115	120	125
Leu Glu Asp Asn Ala Gly Ala Pro Thr Ser Glu Ser Leu Val Val Glu	130	135	140
Ile Asn Glu Arg Lys Asp Pro Leu Val Ser Ser Asp Asn Gly Gly Pro	145	150	155
Pro Pro Pro Pro Val Pro Val Ala Gln Gly Val Ala Thr Ser Asp Glu	165	170	175
Gly Ser Pro Pro Gln Thr Pro Asp Leu Ser Arg Ser Ser Thr Pro Ile	180	185	190
Ser Gly His Leu Leu Thr Ala Lys Gly Gly Pro Ala Gly Arg Ala Ser	195	200	205
Arg Arg Ala Arg Lys Ala Ala Asn Ala Ser Ala Thr Ala Ser Ser Gly	210	215	220
Asp Glu Ser Ile Arg Lys Gly Lys Thr Leu Lys Ser Gly Lys Lys Met	225	230	235
Arg Lys Trp Asp Ala Asp Gly Phe Ala Asp Glu Asp Asp Gly Lys Val	245	250	255
Leu Asp Tyr Ser Ala Pro Ala Asp Gly Glu Asp Ala Pro Ala Pro Val	260	265	270
Val Glu Ala Val Ala Gln Glu Ser Trp Gly Arg Arg Thr Gly Lys Gly	275	280	285
Gln Phe Val Leu Lys Asp Leu Gly Asp Glu Val His Ser Ile Leu Glu	290	295	300
Asn Ala Asp His Glu Lys Thr Lys Ser Ser Ser Ser Thr Gly Phe Val	305	310	315
Gly Ser Gly Val Asn Ala Leu Gly Gly Phe Phe Arg Asn Ile Val Gly	325	330	335
Gly Lys Val Leu Thr Glu Ala Asp Leu Glu Lys Pro Leu Lys Ala Met	340	345	350
Glu Asp His Leu Leu Lys Lys Asn Val Ala Arg Glu Ala Ala Val Arg	355	360	365
Leu Cys Gln Gly Val Gln Arg Glu Leu Val Gly Lys Lys Thr Gly Asn	370	375	380
Phe Gln Ser Val Asp Ala Ala Leu Arg Ser Ala Met Glu Ser Ser Leu	385	390	395
			400

Arg Lys Ile Leu Thr Pro Thr Ser Ser Leu Asp Leu Leu Arg Glu Ile
 405 410 415
 Asp Ala Val Arg Ser Pro Thr Ser Lys Gly Gln Ala Pro Arg Pro Tyr
 420 425 430
 Val Ile Ser Ile Val Gly Val Asn Gly Val Gly Lys Ser Thr Asn Leu
 435 440 445
 Gly Lys Ile Cys Tyr Phe Leu Leu Gln Asn Asn Tyr Arg Val Leu Ile
 450 455 460
 Ala Ala Cys Asp Thr Phe Arg Ser Gly Ala Val Glu Gln Leu Arg Val
 465 470 475 480
 His Ala Arg Asn Leu Lys Glu Leu Ser Thr Arg Glu Asn Ala Gly Glu
 485 490 495
 Val Glu Leu Tyr Glu Lys Gly Tyr Gly Lys Asp Ala Ala Asn Val Ala
 500 505 510
 Lys Asp Ala Val Glu Tyr Gly Ala Ala Asn His Phe Asp Val Val Leu
 515 520 525
 Ile Asp Thr Ala Gly Arg Arg His Asn Asp Gln Arg Leu Met Ser Ser
 530 535 540
 Leu Glu Lys Phe Ala Lys Phe Ala Lys Pro Asp Lys Ile Phe Met Val
 545 550 555 560
 Gly Glu Ala Leu Val Gly Thr Asp Ser Val Met Gln Ala Arg Asn Phe
 565 570 575
 Asn Gln Ala Phe Gly Thr Gly Arg Asn Leu Asp Gly Phe Ile Ile Ser
 580 585 590
 Lys Cys Asp Thr Val Gly Asp Met Val Gly Thr Leu Val Ser Met Val
 595 600 605
 His Ala Thr Gly Ile Pro Ile Val Phe Leu Gly Val Gly Gln His Tyr
 610 615 620
 Gly Asp Leu Arg Gly Leu Ser Val Pro Trp Ala Val Asn Leu Leu Met
 625 630 635 640
 Lys

<210> 127

<211> 2564

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 127

cagcgaaggt atcggagagg agttgaccag aactggggag tagtcatggt tatgagacga 60

aaggtcgacg	gttcagaagg	atTTTTgcgg	gacttgattg	agagttgtga	gcgcgacaga	120
tggattggat	caaggattca	attgatcaga	gctcggctca	gatcatgtat	ccagtcttcc	180
gatgattccg	attattgtga	aactgggtta	aatcgcgcca	gaggggcagg	tatcgtgacg	240
gagagggggt	atatcgtcga	atggagggtt	tgagtgcaga	cggccgacga	ttgcgcagtt	300
caaagcggcg	aagaggtctt	ggcactctcg	gtccaaacac	gttgcccgtt	ctctccaact	360
aaacggaact	gacgaagctc	cttcagagga	cactctcctc	taccgattca	tttccttaat	420
ctattccttc	tctttctccg	gactgcagtg	acttcccttt	cagccaattg	cccgtccac	480
tgtgcggcat	tcgatatacc	atgcggtggt	gcctcactct	tctggcattc	tgcttcttgg	540
cagttgtacg	tgcattaagt	agctccggga	gtcgtctggt	ggttggtttg	gaagatgcca	600
cagaaaagga	attatactcg	aaattatggg	ctgacctaga	aggtgctcta	acctactgaa	660
cttctacggt	aataatgtaa	tattaattgg	tagctcgagg	atataacctc	gacttcgaat	720
ccccaagaa	tgacaagctc	agcctgttcg	aactcggaga	ccgagtctac	gaccacatgc	780
ttctcctgcc	tcccaagtca	aagggttagc	gttaccctta	gacatgtcca	tatgctctgc	840
tttgtacatc	tcaattgacc	tcttgccag	gctatggacc	ctcccttacc	cccaagaata	900
tcattgattt	catgaacaag	gacggtaacg	tcctcctcgc	cttgtcgggc	aagtccacaa	960
ccgccagcgc	tatcagctcg	ctgctattgg	agctcgatct	ccatctccct	gtcgcagctt	1020
cctctgtcac	cgtcgatcac	ttcaactacg	atacactttc	tgctccgat	aagcatgatg	1080
ttctgctact	ccaccgacca	ggcaagttga	ggtccgatac	caaggctttc	tttgatggcg	1140
agggcggtgt	agcatttccc	agagccgtcc	cccacacct	ggcgatgca	aacctctca	1200
ttgcgcctat	tctgcgagcg	cccgccactg	cgtatagtta	caaccccaag	gaggacgcgt	1260
cgtcagttga	ggatgttgca	gctacgggtt	cgcagttggc	tctggtctcg	gccatgcagg	1320
ctagaaaactc	cgctcggttc	actctactgg	gatccgtgga	gagtctgcag	gatcagtggt	1380
tttctgcgac	tgtcaaggct	cctgggtgatg	ggaagcagat	gaagacggtc	aaccaggaat	1440
tcgccaagca	gcttactgcg	tggacattca	aggaaaccgg	agtcctcaag	gtcggaaaga	1500
tcgagcatca	tctggctgaa	gatggtgaaa	tactcccga	gaagctgaac	cctaagatct	1560
atcgaataaa	gaatgaaact	gtaagtgaca	gccatctgag	gttccattgc	ctatttgcac	1620
gctcaccctt	ctcaacaggt	ctttagcatt	gaactttccg	aatacaacta	tgatcgttac	1680
gcgccttctg	aggttccaac	tggcgatgcc	gtccagctcg	agtttaccat	gctgtctccc	1740
ttccatcgcc	tgaacttgga	accgctccgt	cgaacagata	acagtacagt	ttacagcaca	1800
cgattcacca	cccccgatca	gcatggaatc	ttctccttcc	gagtgaacta	caagcgcccg	1860
ttctcacga	acatcgaaga	aaaacttgag	gtgaccgttc	gtcatttccg	tcataacgag	1920
tacccccgaa	gctggaaaat	cagcgggtgga	tgggtctgga	ttgcgggtct	gtgggtccgtc	1980
atcgctggct	tcttagtatt	cgttggtgca	tggctttact	cagcgcttcc	tgccgccgca	2040
ctgaacacaa	agaagacaca	ataatcctct	atagaatctc	aacgaatgat	acttcggaat	2100
gaagcgtgca	cttacgccgg	aagcccataa	ttcaaaaagta	tgtacagtca	tatgccataa	2160
gctagtagtg	ttacatgaaa	tccggaatct	caagacattc	cgccaactgg	gaactccaaa	2220
accatgccag	gagatgagat	aaaaagccgc	acaataactc	agaacagcgg	atctaggcat	2280
ctggccagcc	tagtgagccg	cgagcttgaa	aatttatagt	cctctagtct	tctcagggtc	2340
catctgaact	tcattcccgc	tgatctcctt	aacggtttcg	aaggcgggct	tgccggcgta	2400
tagttgctgg	tgggattggg	atttgccctc	ttcgagctcc	ctggaaaccg	agataggctg	2460
atttccacgg	aatcgctttc	gcatgtcgat	caaccacgc	ctagattgtg	cccgttgtca	2520
gcactatcca	atgtaattaa	agcacgcata	tccgttccac	ccac		2564

<210> 128

<211> 1564

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
Genomic sequence containing the coding region

<400> 128

atgcggtggt	gcctcactct	tctggcattc	tgttcttgg	cagttgtacg	tgcattaagt	60
agctccggca	gtcgtctggt	ggttggtttg	gaagatgcc	cagaaaagga	attatactcg	120
aaattatggg	ctgacctaga	aggtgctcta	acctactgaa	cttctacgtt	aataatgctaa	180
tattaattgg	tagctcgagg	atataacctc	gacttcgaat	ccccaagaa	tgacaagctc	240
agcctgttcg	aactcggaga	ccgagtctac	gaccacatgc	ttctcctgcc	tcccaagtca	300
aagggttagc	gttaccctta	gacatgtcca	tatgctctgc	tttgtacatc	tcaattgacc	360
tcttgccag	gctatggacc	ctcccttacc	cccaagaata	tcattgattt	catgaacaag	420

```

gacggtaacg tcctcctcgc cttgtcgggc aagtccacaa ccgccagcgc tatcagctcg 480
ctgctattgg agctcgatct ccactcctct gtcgatcggt cctctgtcac cgtcgatcac 540
ttcaactacg atacactttc tgccctccgat aagcatgatg ttctgctact ccaccgacca 600
ggcaagttga ggtccgatac caaggctttc tttgatggcg agggcgttgt agcatttccc 660
agagccgtcc cccacaccct gggcgatgca aaccctctca ttgcgctat tctgcgagcg 720
cccgccactg cgtatagtta caaccccaag gaggacgcgt cgtcagttga ggatgttgca 780
gctacgggtt cgcagttggc tctggctctc gccatgcagg ctagaaactc cgctcgggtc 840
actctactgg gatccgtgga gagtctgcag gatcagtggt tttctgcgac tgtcaaggct 900
cctggtgatg ggaagcagat gaagacggtc aaccaggaat tcgccaagca gcttactgcg 960
tggacattca aggaaccgg agtcctcaag gtcggaaaga tcgagcatca tctggctgaa 1020
gatggtgaaa tcactcccga gaagctgaac cctaagatct atcgaataaa gaatgaaact 1080
gtaagtgaac gccatctgag gttccattgc ctatttgcag gctcaccctt ctcaacaggt 1140
cttttagcatt gaactttccg aatacaacta tgatcggtac gcgcccttcg aggttccaac 1200
tggcgatgcc gtccagctcg agtttaccat gctgtctccc ttccatcgcc tgaaacttga 1260
acccgtccgt cgaacagata acagtacagt ttacagcaca cgattcacca ccccgatca 1320
gcatggaatc ttctccttcc gagtgaacta caagcgcccg ttccctacga acatcgaaga 1380
aaaacttgag gtgaccgttc gtcatttctc tcataacgag tacccccga gctggaaaat 1440
cagcggtgga tgggtctgga ttgcggtctc gtggtccgtc atcgctggct tcttagtatt 1500
cgttgttgca tggctttact cagcgccttc tgccgcccga ctgaacacaa agaagacaca 1560
ataa 1564

```

<210> 129

<211> 1383

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
Coding region without introns

<400> 129

```

atgcggtggt gcctcactct tctggcattc tgcttcttgg cagttgtacg tgcattaagt 60
agctccggca gtcgtctgtt ggttggtttg gaagatgcca cagaaaagga attatactcg 120
aaattatggg ctgacctaga aggatataac ctgcacttcg aatcccccaa gaatgacaag 180
ctcagcctgt tcgaactcgg agaccgagtc tacgaccaca tgcttctcct gcctcccaag 240
tcaaagggtc atggaccctc ccttaccccc aagaatatca ttgatttcat gaacaaggac 300
ggtaacgtcc tcctcgctt gtgaggcaag tccacaaccg ccagcgctat cagctcgctg 360
ctattggagc tcgatctcca tctccctgtc gatcggttct ctgtcaccgt cgatcacttc 420
aactacgata cactttctgc ctccgataag catgatgttc tgctactcca ccgaccaggc 480
aagttgaggt ccgataccaa ggctttcttt gatggcgagg gcgttgtagc atttcccaga 540
gccgtccccc acaccctggg cgatgcaaac cctctcattg cgctattct gcgagcgccc 600
gccactgcgt atagttacaa cccaaggag gacgcgtcgt cagttgagga tgttgagct 660
acgggttcgc agttggctct ggtctcggcc atgcaggcta gaaactccgc tcggttact 720
ctactgggat ccgtggagag tctgcaggat cagtgtttt ctgcgactgt caaggctcct 780
ggtgatggga agcagatgaa gacggtcaac caggaattcg ccaagcagct tactgcgtgg 840
acattcaagg aaaccggagt cctcaaggtc ggaaagatcg agcatcatct ggctgaagat 900
ggtgaaatca ctcccagaaa gctgaaccct aagatctatc gaataaagaa tgaaactgtc 960
tttagcattg aactttccga atacaactat gatcgttacg cgcccttcca ggttccaact 1020
ggcgatgccg tccagctcga gtttaccatg ctgtctccct tccatcgctt gaacttggaa 1080
cccgtccgtc gaacagataa cagtacagtt tacagcacac gattcaccac ccccgatcag 1140
catggaatct tctccttccg agtgaactac aagcgcccggt tcctcacgaa catcgaagaa 1200
aaacttgagg tgaccgttcg tcatttctgt cataccagat acccccgaag ctggaaaatc 1260
agcgggtggat ggggtctggat tgcgggtctg tggctccgtc tcgctggctt cttagtattc 1320
gttgttgcat ggctttactc agcgccttct gccgcccgcac tgaacacaaa gaagacacaa 1380
taa 1383

```

<210> 130

<211> 460

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
Protein sequence

<400> 130

Met Arg Trp Cys Leu Thr Leu Leu Ala Phe Cys Phe Leu Ala Val Val
1 5 10 15

Arg Ala Leu Ser Ser Ser Gly Ser Arg Leu Leu Val Val Leu Glu Asp
20 25 30

Ala Thr Glu Lys Glu Leu Tyr Ser Lys Leu Trp Ala Asp Leu Glu Gly
35 40 45

Tyr Asn Leu Asp Phe Glu Ser Pro Lys Asn Asp Lys Leu Ser Leu Phe
50 55 60

Glu Leu Gly Asp Arg Val Tyr Asp His Met Leu Leu Leu Pro Pro Lys
65 70 75 80

Ser Lys Gly Tyr Gly Pro Ser Leu Thr Pro Lys Asn Ile Ile Asp Phe
85 90 95

Met Asn Lys Asp Gly Asn Val Leu Leu Ala Leu Ser Gly Lys Ser Thr
100 105 110

Thr Ala Ser Ala Ile Ser Ser Leu Leu Leu Glu Leu Asp Leu His Leu
115 120 125

Pro Val Asp Arg Ser Ser Val Thr Val Asp His Phe Asn Tyr Asp Thr
130 135 140

Leu Ser Ala Ser Asp Lys His Asp Val Leu Leu Leu His Arg Pro Gly
145 150 155 160

Lys Leu Arg Ser Asp Thr Lys Ala Phe Phe Asp Gly Glu Gly Val Val
165 170 175

Ala Phe Pro Arg Ala Val Pro His Thr Leu Gly Asp Ala Asn Pro Leu
180 185 190

Ile Ala Pro Ile Leu Arg Ala Pro Ala Thr Ala Tyr Ser Tyr Asn Pro
195 200 205

Lys Glu Asp Ala Ser Ser Val Glu Asp Val Ala Ala Thr Gly Ser Gln
210 215 220

Leu Ala Leu Val Ser Ala Met Gln Ala Arg Asn Ser Ala Arg Phe Thr
225 230 235 240

Leu Leu Gly Ser Val Glu Ser Leu Gln Asp Gln Trp Phe Ser Ala Thr
245 250 255

Val Lys Ala Pro Gly Asp Gly Lys Gln Met Lys Thr Val Asn Gln Glu
260 265 270

Phe Ala Lys Gln Leu Thr Ala Trp Thr Phe Lys Glu Thr Gly Val Leu
275 280 285

Lys Val Gly Lys Ile Glu His His Leu Ala Glu Asp Gly Glu Ile Thr
 290 295 300
 Pro Glu Lys Leu Asn Pro Lys Ile Tyr Arg Ile Lys Asn Glu Thr Val
 305 310 315 320
 Phe Ser Ile Glu Leu Ser Glu Tyr Asn Tyr Asp Arg Tyr Ala Pro Phe
 325 330 335
 Glu Val Pro Thr Gly Asp Ala Val Gln Leu Glu Phe Thr Met Leu Ser
 340 345 350
 Pro Phe His Arg Leu Asn Leu Glu Pro Val Arg Arg Thr Asp Asn Ser
 355 360 365
 Thr Val Tyr Ser Thr Arg Phe Thr Thr Pro Asp Gln His Gly Ile Phe
 370 375 380
 Ser Phe Arg Val Asn Tyr Lys Arg Pro Phe Leu Thr Asn Ile Glu Glu
 385 390 395 400
 Lys Leu Glu Val Thr Val Arg His Phe Ala His Asn Glu Tyr Pro Arg
 405 410 415
 Ser Trp Lys Ile Ser Gly Gly Trp Val Trp Ile Ala Gly Leu Trp Ser
 420 425 430
 Val Ile Ala Gly Phe Leu Val Phe Val Val Ala Trp Leu Tyr Ser Ala
 435 440 445
 Pro Ser Ala Ala Ala Leu Asn Thr Lys Lys Thr Gln
 450 455 460

<210> 131

<211> 3376

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 131

gccagggcaa	catctacctt	atggcatcgc	agagcgagaa	ttgctcaaca	tctttgaggt	60
ctttctgctt	gaattcccgg	ggacccttct	tctccttctt	gctcttcgcc	ttggcctttt	120
tatttcgggc	ctgagcattg	ctcttggtct	ctcggaacctg	ttggtgaaag	ctcgaaagca	180
aaggcgccat	tggtctttgt	cgaagaggca	attgacatgt	tgagagaaatg	ctccttgccg	240
ccgacggcag	gatcgagccg	aaggaggaca	tggtttgaag	agtggattga	tgcgagcttt	300
cagactaact	cctgggagac	ggagatgttt	tcttctccga	aagctctctc	tcagtgatgc	360
gggcaggaga	aacgtaacgc	cggcggagtc	ccttttgagt	cagatgcccc	tctgtactat	420
tcaattttcg	gggaattcaa	cagcccactt	gttacgctct	cgcaggtcga	tttcaactcg	480
ggcggatttt	gagggccgca	atgtctcagt	atcagcttac	tgtggccacc	agggccaatc	540
agccctatgt	acttcctgtc	ctactggctg	caacttccat	caacgaggca	cgaccaagcc	600
cagtgatatc	gatcacctat	gaggatactg	cggttcttcg	tgaaggagac	aaggccgtcg	660
tgcaatacac	tggagctagc	ggtaatccta	tctttggcct	tatcaatgct	gttcaggaac	720
tccgcaaaga	cttccccttc	cttaacagca	aggatgagaa	gctggtaaga	ggcgccatgg	780
agccttactg	ctgatgagca	ctgataagtg	atactaacc	tccttttata	ggagaatgaa	840
tggtgtgtct	agttggaagc	atttgctcct	ctagatttca	aggcccttga	ccctgaattg	900
cagcgccctg	ataccacact	cctgctgaga	tctttcgtcg	tcggttacgc	tctctcgacg	960

gccgacattg	ccctttgggg	tgccatccga	ggcaaccgtg	tgcgagttgc	cgcgatcaag	1020
aagggctcac	ttgtcaatgt	gactcggttg	ttctatttct	tggaggatct	gtgcccgtgg	1080
gccacatcta	cactggaggt	cttgaaccag	gctgtgagag	agaagaaggc	cgccaaggcg	1140
aaggaggag	ctagctacga	catcgctctt	ctcaacactg	aaaaaggcgt	ggtgacaagg	1200
tttcctcccg	agccttcagg	ttatcttcac	atcggtcacg	caaaagctgc	gctgctcaac	1260
gactactttg	cccacgagaa	gtataatggc	acccttcttg	tccgctttga	cgacacaaat	1320
ccttcgaacg	agaagctcga	gttccaggac	gcgatcattg	aagatccttg	tctcatgggc	1380
atcaagcccg	acaagatgag	ctacaccagt	gactactttg	acgagcttta	ccagtacgcc	1440
cttcaaataca	tcaaggacgg	taacgcctac	gccgacgata	ccgagaagga	ggtcatggct	1500
gagcagagaa	tgaatggaaa	acccagcaag	cgctcgtagt	catccgtcga	ggagaacctt	1560
gcccgccttcg	aggagatgaa	gaagggtacc	ctgaggggtc	tccgttggtg	tatccgagcc	1620
aagatgctctg	tcgataaccc	caacaaggcc	atgctgtatc	ctgtcattta	ccgctgcaac	1680
cctgcccctc	accaccgcac	tgggacgaag	tggaagatct	atcctaccta	tgacttcgcc	1740
tgccctatcg	tcgattcaat	tgagggtgtg	actcatgccc	tcagaacat	tgaataccgc	1800
gatcgcaacc	ctcagtacca	gtggttcttg	gacacgctca	agcttcgcca	tgtccaaatc	1860
tgggattttg	ctcgcatgaa	cttcattcgc	accttgctgt	ctaagagaaa	acttaccaag	1920
ctcgtaaac	aagggtgctg	ctggggatgg	gatgagtaag	tttacctttg	cttgcaaacg	1980
gattcttctg	ttactaacga	tgtcagtcct	cgtttcccca	ccatccgagt	aagtaacatg	2040
cctagtcatg	cctgcgaatc	cccttattca	tccggcattt	tttaccatct	cacctacttc	2100
ccatgtactg	ttactgtccc	acgctaattc	tttcataggg	catccgacga	aggggaatga	2160
ctatccctgc	tctgagagaa	ttcattctta	agcagggacc	cagcaagaac	atcaccaacc	2220
ttgactggac	cctgatctgg	gcgaccaaca	agaagtacat	tgatcctgtc	gcacctcgtc	2280
acactgccat	tctcaagaag	gatatggtca	aggcgatcgt	caaggagggc	ccggctacac	2340
cttacacgga	agagaaacct	aagcacggca	agaaccctgc	agttggtatg	aagaagggtg	2400
tttttggtaa	cacggtcatt	ttcgaccaga	aagatgccaa	gagcttcaag	caagatgaag	2460
agatcacctt	gatgagctgg	ggtaatgcc	ttgtccgtaa	gatcgagacc	gacacctacc	2520
caggcatcgt	caaggagctg	gagctggagc	tccacctgga	aggtgacttc	aaaaagaccg	2580
agaagaagg	cacgtggctc	tctactgag	gacaggacct	aattcccgtt	gaattggctg	2640
atttcgacta	tctcctcaac	aaggacacc	tgcaggagga	cgacgtcctt	gaggatgtcc	2700
tgaacaagaa	accgagtttc	agagaggacg	ctgttgctga	ctgcaacgtc	gctgaactga	2760
aagaagggtga	catcatccag	tttgagcgca	agggctatta	ccgtgttgac	cgggcctatg	2820
taccgggcaa	gccggctgtt	ttgttcaaca	ttcccacggg	caagacgggc	aaatagatga	2880
atagtctgat	atttgggact	taacgaagcc	acgcatgtgt	ctacaacgct	gtagatatta	2940
gaagcactga	aagagaattc	aatttacatt	gttaggatgc	taaatacgctg	atttacgaca	3000
ggtgtaagtc	ttgttaattg	caagaatacc	agtacttata	gttatttccc	ttcttctttg	3060
cagcaacgat	accttgatgc	tccctacaag	gaagcttaca	caatatgggtc	taagggtgtg	3120
tctatctata	cgccatacta	gctgcccggg	tctgcgctac	ccgcccatac	gcgccatctt	3180
ctactccgta	caatctccac	aatttctccc	agctgcattg	agatgtgatt	ccatgagaag	3240
cgaaagatga	tcttcatgac	gtcgaagact	aaactacctt	acctcttggtc	cggacacgag	3300
ccatccggcg	agaaccgaca	gcgttggttc	atggcttact	agttggcctg	tggatcatcgt	3360
ctacttgatc	atcttt					3376

<210> 132

<211> 2376

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737
 Genomic sequence containing the coding region

<400> 132

atgtctcagt	atcagcttac	tgtggccacc	agggccaatc	agccctatgt	acttctgtgc	60
ctactggctg	caacttccat	caacgaggca	cgaccaagcc	cagtgatatc	gatcacctat	120
gaggatactg	cggttcttcg	tgaaggagac	aaggccgtcg	tgcaatacac	tggagctagc	180
ggtaatccta	tctttggcct	tatcaatgct	gttcagggaac	tccgcaaaga	cttccccttc	240
cttaacagca	aggatgagaa	gctggtaaga	ggcgccatgg	agccttactg	ctgatgagca	300
ctgataagtg	atactaacc	tccttttata	ggagaatgaa	tggctgtctc	agttggaagc	360
atttgctcct	ctagatttca	aggcccttga	ccctgaattg	cagcgccctg	ataccacact	420
cctgctgaga	tctttcgtcg	tcggttacgc	tctctcgacg	gccgacattg	ccctttgggg	480

tgccatccga	ggcaaccgtg	tgcgagttgc	cgcgatcaag	aagggctcac	ttgtcaatgt	540
gactcggttg	ttctatttct	tggaggatct	gtgcccgtgg	gccacatcta	cactggaggt	600
cttgaaccag	gctgtgcgag	agaagaaggc	cgccaagcg	aaggagggag	ctagctacga	660
catcgctctt	ctcaacactg	aaaaagcggt	ggtgacaagg	tttcctccc	agccttcagg	720
ttatcttcac	atcggtcacg	caaaagctgc	gctgctcaac	gactactttg	cccacgagaa	780
gtataatggc	acccttcttg	tccgctttga	cgacacaaat	ccttcgaacg	agaagctcga	840
gttccaggac	gcgatcattg	aagatcttgc	tctcatgggc	atcaagcccc	acaagatgag	900
ctacaccagt	gactactttg	acgagcttta	ccagtacgcc	cttcaaata	tcaaggacgg	960
taacgcctac	gccgacgata	ccgagaagga	ggtcatggct	gagcagagaa	tgaatggaaa	1020
acccagcaag	cgctcgatg	catccgtcga	ggagaacctt	gcccgcctcg	aggagatgaa	1080
gaagggtacc	cctgagggtc	tccgttgggt	tatccgagcc	aagatgtctg	tcgataaccc	1140
caacaaggcc	atgcgtgata	ctgtcattta	ccgctgcaac	cctgccccctc	accaccgcac	1200
tgggacgaag	tggaagatct	atcctaccta	tgacttcgcc	tgccctatcg	tcgattcaat	1260
tgagggtgtg	actcatgccc	tcagaaccaa	tgaataccgc	gatcgcaacc	ctcagtagca	1320
gtgggttctt	gacacgctca	agcttcgcca	tgtccaaatc	tgggattttg	ctcgcagtaa	1380
cttcatttgc	accttgctgt	ctaagagaaa	acttaccaag	ctcgttaacc	aaggtgtcgt	1440
ctggggatgg	gatgagtaag	tttacctttg	cttgcaaacg	gattcttgtc	ttactaacga	1500
tgtcagtcct	cgtttcccca	ccatccgagt	aagtaacatg	cctagtcatg	cctgcgaatc	1560
cccttattca	tccggcattt	tttaccatct	cacctacttc	ccatgtactg	ttacttccc	1620
acgctaatac	tttcataggg	catccgacga	aggggaatga	ctatccctgc	tctgagagaa	1680
ttcattctta	agcagggacc	cagcaagaac	atcaccaacc	ttgactggac	cctgatctgg	1740
gcgaccaaca	agaagtacat	tgatcctgtc	gcacctcgtc	acactgccat	tctcaagaag	1800
gatattggtc	aggcgatcgt	caaggagggc	ccggctacac	cttacacgga	agagaaacct	1860
aagcacggca	agaaccctgc	agttggtatg	aagaagggtg	tttttggtaa	cacggtcatt	1920
ttcgaccaga	aagatgccaa	gagcttcaag	caagatgaag	agatcacctt	gatgagctgg	1980
ggtaatgcc	ttgtccgtaa	gatcgagacc	gatcctacct	caggcatcgt	caaggagctg	2040
gagctggagc	tccacctgga	aggtgacttc	aaaaagaccg	agaagaaggt	cacgtggctc	2100
tctactgagc	gacaggacct	aattcccgtt	gaattggtcg	atttcgacta	tctcctcaac	2160
aaggacaccc	tcgaggagga	cgacgtcctt	gaggatgtcc	tgaacaagaa	caccgagttc	2220
agagaggacg	ctgttgctga	ctgcaacgtc	gctgaactga	aagaagggtg	catcatccag	2280
tttgagcgca	agggtctatta	ccgtgttgac	cgggcctatg	taccgggcaa	gccggctgtt	2340
ttgttcaaca	ttcccacggg	caagacgggc	aaatag			2376

<210> 133

<211> 2148

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737

Coding region without introns

<400> 133

atgtctcagt	atcagcttac	tgtggccacc	agggccaatc	agccctatgt	acttcctgtc	60
ctactgggtc	caacttccat	caacgaggca	cgaccaagcc	cagtgatata	gatcacctat	120
gaggatactg	cggttcttcg	tgaaggagac	aaggccgtcg	tgcaatacac	tggagctagc	180
ggtaatccta	tctttggcct	tatcaatgct	gttcaggaac	tccgcaaaga	cttccccttc	240
cttaacagca	aggatgagaa	gctggagaat	gaatggctgt	ctcagttgga	agcatttgct	300
cctctagatt	tcaaggccct	tgaccctgaa	ttgcagcgcc	tcgataccca	cctcctgctg	360
agatctttcg	tcgtcggtta	cgctctctcg	acggccgaca	ttgccctttg	gggtgccatc	420
cgaggcaaac	gtgtcgcagt	tgccgcgata	aagaagggtc	cacttgtcaa	tgtgactcgt	480
tggttctatt	tcttgaggaa	tctgtgcccg	tgggccacat	ctacactgga	ggtcttgaa	540
caggctgtgc	gagagaagaa	ggccgccaag	gcgaaggagg	gagctagcta	cgacatcgct	600
cttctcaaca	ctgaaaaagg	cgtggtgaca	aggtttcctc	ccgagccttc	aggttatctt	660
cacatcggtc	acgcaaaagc	tgcgctgctc	aacgactact	ttgcccacga	gaagtataat	720
ggcacccttc	ttgtccgctt	tgacgacaca	aatccttcga	acgagaagct	cgagttccag	780
gacgcgatca	ttgaagatct	tgctctcatg	ggcatcaagc	ccgacaagat	gagctacacc	840
agtgactact	ttgacgagct	ttaccagtag	gcccttcaaa	tcatcaagga	cggtaacgcc	900
tacgccgacg	ataccgagaa	ggaggtcatg	gctgagcaga	gaatgaatgg	aaaaccagc	960
aagcgctcgt	atgcatccgt	cgaggagaac	cttgcccgtc	tcgaggagat	gaagaagggt	1020

```

acccttgagg gtctccgttg gtgtatccga gccaatgatgt ctgtcgataa ccccaacaag 1080
gccatgcgtg atcctgtcat ttaccgctgc aaccctgccc ctcaccaccg cactgggacg 1140
aagtgggaaga tctatcctac ctatgacttc gcctgcccta tcgtcgattc aattgagggg 1200
gtgactcatg ccctcagaac cattgaatac cgcgatcgca accctcagta ccagtgggtc 1260
ttggacacgc tcaagcttcg ccatgtccaa atctgggatt ttgctcgcat gaacttcatt 1320
cgcaccttgc tgtctaagag aaaacttacc aagctcggtt accaagggtg cgtctgggga 1380
tgggatgatc ctcgtttccc caccatccga ggcacccgac gaaggggaat gactatccct 1440
gctctgagag aattcattct taagcaggga cccagcaaga acatcaccaa ccttgactgg 1500
accctgatct gggcgaccaa caagaagtac attgatcctg tcgcacctcg tcacactgcc 1560
attctcaaga aggatatggt caaggcgatc gtcaaggag gcccggctac accttacacg 1620
gaagagaaac ctaagcacgg caagaacct gcagttggta tgaagaagg ggtttttggt 1680
aacacgggtca ttttcgacca gaaagatgcc aagagcttca agcaagatga agagatcacc 1740
ttgatgagct ggggtaaatgc cattgtccgt aagatcgaga ccgatcctac ctcaggcatc 1800
gtcaaggagc tggagctgga gctccacctg gaagggtgact tcaaaaagac cgagaagaag 1860
gtcacgtggc tctctactga gggacaggac ctaattcccg ttgaattggt cgatttcgac 1920
tatctcctca acaaggacac cctgcaggag gacgacgtcc ttgaggatgt cctgaacaag 1980
aacaccgagt tcagagagga cgctgttgct gactgcaacg tcgctgaact gaaagaagg 2040
gacatcatcc agtttgagcg caagggctat taccgtgttg accgggccta tgtaccgggc 2100
aagccggctg ttttgttcaa cattcccacg ggcaagacgg gcaaatag 2148

```

<210> 134

<211> 715

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737
Protein sequence

<400> 134

```

Met Ser Gln Tyr Gln Leu Thr Val Ala Thr Arg Ala Asn Gln Pro Tyr
1          5          10          15

Val Leu Pro Val Leu Leu Val Ala Thr Ser Ile Asn Glu Ala Arg Pro
20        25        30

Ser Pro Val Ile Ser Ile Thr Tyr Glu Asp Thr Ala Val Leu Arg Glu
35        40        45

Gly Asp Lys Ala Val Val Gln Tyr Thr Gly Ala Ser Gly Asn Pro Ile
50        55        60

Phe Gly Leu Ile Asn Ala Val Gln Glu Leu Arg Lys Asp Phe Pro Phe
65        70        75        80

Leu Asn Ser Lys Asp Glu Lys Leu Glu Asn Glu Trp Leu Ser Gln Leu
85        90        95

Glu Ala Phe Ala Pro Leu Asp Phe Lys Ala Leu Asp Pro Glu Leu Gln
100       105       110

Arg Leu Asp Thr His Leu Leu Leu Arg Ser Phe Val Val Gly Tyr Ala
115       120       125

Leu Ser Thr Ala Asp Ile Ala Leu Trp Gly Ala Ile Arg Gly Asn Arg
130       135       140

Val Ala Val Ala Ala Ile Lys Lys Gly Ser Leu Val Asn Val Thr Arg

```

145		150		155		160
Trp Phe Tyr Phe	Leu Glu Asp Leu Cys	Pro Trp Ala Thr Ser Thr Leu				
	165	170			175	
Glu Val Leu Asn Gln Ala Val Arg Glu Lys Lys Ala Ala Lys Ala Lys						
	180	185			190	
Glu Gly Ala Ser Tyr Asp Ile Ala Leu Leu Asn Thr Glu Lys Gly Val						
	195	200			205	
Val Thr Arg Phe Pro Pro Glu Pro Ser Gly Tyr Leu His Ile Gly His						
	210	215			220	
Ala Lys Ala Ala Leu Leu Asn Asp Tyr Phe Ala His Glu Lys Tyr Asn						
	225	230			235	240
Gly Thr Leu Leu Val Arg Phe Asp Asp Thr Asn Pro Ser Asn Glu Lys						
	245	250			255	
Leu Glu Phe Gln Asp Ala Ile Ile Glu Asp Leu Ala Leu Met Gly Ile						
	260	265			270	
Lys Pro Asp Lys Met Ser Tyr Thr Ser Asp Tyr Phe Asp Glu Leu Tyr						
	275	280			285	
Gln Tyr Ala Leu Gln Ile Ile Lys Asp Gly Asn Ala Tyr Ala Asp Asp						
	290	295			300	
Thr Glu Lys Glu Val Met Ala Glu Gln Arg Met Asn Gly Lys Pro Ser						
	305	310			315	320
Lys Arg Arg Asp Ala Ser Val Glu Glu Asn Leu Ala Arg Phe Glu Glu						
	325	330			335	
Met Lys Lys Gly Thr Pro Glu Gly Leu Arg Trp Cys Ile Arg Ala Lys						
	340	345			350	
Met Ser Val Asp Asn Pro Asn Lys Ala Met Arg Asp Pro Val Ile Tyr						
	355	360			365	
Arg Cys Asn Pro Ala Pro His His Arg Thr Gly Thr Lys Trp Lys Ile						
	370	375			380	
Tyr Pro Thr Tyr Asp Phe Ala Cys Pro Ile Val Asp Ser Ile Glu Gly						
	385	390			395	400
Val Thr His Ala Leu Arg Thr Ile Glu Tyr Arg Asp Arg Asn Pro Gln						
	405	410			415	
Tyr Gln Trp Phe Leu Asp Thr Leu Lys Leu Arg His Val Gln Ile Trp						
	420	425			430	
Asp Phe Ala Arg Met Asn Phe Ile Arg Thr Leu Leu Ser Lys Arg Lys						
	435	440			445	
Leu Thr Lys Leu Val Asn Gln Gly Val Val Trp Gly Trp Asp Asp Pro						
	450	455			460	
Arg Phe Pro Thr Ile Arg Gly Ile Arg Arg Arg Gly Met Thr Ile Pro						
	465	470			475	480

Ala Leu Arg Glu Phe Ile Leu Lys Gln Gly Pro Ser Lys Asn Ile Thr
485 490 495

Asn Leu Asp Trp Thr Leu Ile Trp Ala Thr Asn Lys Lys Tyr Ile Asp
500 505 510

Pro Val Ala Pro Arg His Thr Ala Ile Leu Lys Lys Asp Met Val Lys
515 520 525

Ala Ile Val Lys Gly Gly Pro Ala Thr Pro Tyr Thr Glu Glu Lys Pro
530 535 540

Lys His Gly Lys Asn Pro Ala Val Gly Met Lys Lys Val Val Phe Gly
545 550 555 560

Asn Thr Val Ile Phe Asp Gln Lys Asp Ala Lys Ser Phe Lys Gln Asp
565 570 575

Glu Glu Ile Thr Leu Met Ser Trp Gly Asn Ala Ile Val Arg Lys Ile
580 585 590

Glu Thr Asp Pro Thr Ser Gly Ile Val Lys Glu Leu Glu Leu Glu Leu
595 600 605

His Leu Glu Gly Asp Phe Lys Lys Thr Glu Lys Lys Val Thr Trp Leu
610 615 620

Ser Thr Glu Gly Gln Asp Leu Ile Pro Val Glu Leu Val Asp Phe Asp
625 630 635 640

Tyr Leu Leu Asn Lys Asp Thr Leu Gln Glu Asp Asp Val Leu Glu Asp
645 650 655

Val Leu Asn Lys Asn Thr Glu Phe Arg Glu Asp Ala Val Ala Asp Cys
660 665 670

Asn Val Ala Glu Leu Lys Glu Gly Asp Ile Ile Gln Phe Glu Arg Lys
675 680 685

Gly Tyr Tyr Arg Val Asp Arg Ala Tyr Val Pro Gly Lys Pro Ala Val
690 695 700

Leu Phe Asn Ile Pro Thr Gly Lys Thr Gly Lys
705 710 715

<210> 135

<211> 3639

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 135

```

acgcttttcg cttgtcatat tcaactctag accggttttc atctcccgat atgccttttt      60
gatttcctt ggaggctctt gctttgcctg gagggcggtca cgagtcctgg acgtcatcca      120
ttcactttgg cttcgacacg gcctcacctc ggagtcgaaa tctggaattc acaacgtgag      180
ggtggccaga ccgatgaaag gatattgtaa cgctgcaatt gcttactcca aaccgtagct      240

```

ctttgtgccc	tatcctttgt	tgtgctggac	gtggactact	agtctccgca	ttaaaaggga	300
aacttttgcg	tcgtcggttc	ctcaccttgt	ttgtcgacac	gtccgagact	taatcatccg	360
aaaagaacgg	cctgcgatca	cggccgacct	catgctcgcc	tatcgctcga	gactatcccc	420
tcaccgactc	tgacccgcgt	accctggcct	cacaacacca	acacttctcc	tctagtttcg	480
cgtacctaga	acacgcaaac	atgtcgccat	caatatccta	catttcaggc	cagcttaggc	540
agctaataata	ctatcatctc	gataacaatt	tgtgccgtaa	tgcgctgttc	ctcgccggtc	600
gtttacatgc	ttacgagccc	cgaacggcgg	aagcgtcgta	tttactcgct	ctctgccatc	660
ttcagaacgg	gcaagtcaaa	gccgcatacg	attacagcag	gaattttgga	tcgagaggca	720
cccacctcgg	ctgctcctat	gtcttcgcgc	aagcgtgctt	ggacctagga	aagtatctgg	780
aaggatatcac	agcgttagag	cggagtaaag	gcctttgggc	ttcgaagaac	cactggagta	840
agtattccat	gcgctgatac	ttgcagtcga	cctgcattta	tttcgttgct	ttctgttact	900
gacacatttc	caccttgtgc	tctagataag	cacagtgaga	cgcaagaca	acatctgccg	960
gatgcagccg	cagtattctg	cctgttaggt	aaattatggc	atgcgcataa	ggacatcaac	1020
aaagctgtgg	aatgctatgt	tgaatctctg	aagctgaatc	ccttcatgtg	ggatgcgttc	1080
caagggttgt	gcgacaccgg	taagctttgg	agaataaacc	taatacatct	agccatggct	1140
aattgtgttc	taccgccaa	gagtcaatgt	ccgcgtgtca	aacatctaca	agttgaattc	1200
tgaattgctg	gccgtattgt	cttcacgcgc	acaggcggat	gctgagccaa	tatccgataa	1260
gtctgcacac	acgaatgggc	cactgcaagc	gcaggcgaat	gttaatccaa	gttccgatcc	1320
ttttgcctcg	actacttctc	gcagtgattc	aggtaccagc	catgggagct	ctgccttgtg	1380
ggaaaaacta	aatggaagca	cagtaagcgt	ggcgtcatcg	ggagtgccag	catcaatcgt	1440
gcatgaagga	gccgaaacgc	cgagtgggtc	aagcagcggg	tctgatgagt	tccggttagc	1500
taacggaatg	aacggcgcg	atgcttcttg	ggaccctcct	ttagctcctg	caaggaaaaa	1560
cagaacgatc	caggcaataa	gcggcgagta	tccaatggac	cctcctccca	agatgaaacc	1620
cactgggatc	cgaccaagga	caaggaccag	gactgagccg	gaggacccaa	tttcagccca	1680
gatagaccgg	gaggcaacaa	atgcgcccag	ggtcggggac	cgaaaacgaa	ctgtttcttg	1740
tcaggtagcg	catccaccga	cgtcacaaac	cacagaacca	ggagcacccc	agcggcgag	1800
tgtgcgactc	ttcaaccaga	ttaaaccacc	gaccagcaaa	ttgtcgcgct	ccgcgtggg	1860
agtcaaggat	gctagagaag	tcaagaaagc	gaaagccaca	ggtacgaagg	ggcgtacgac	1920
aaccaccacc	atgggacgag	tagtgagtgg	cagccgaaaa	catgccagcg	aacatcatga	1980
tgcagatggt	aaagacggac	ggtcgggtacc	gtccgcccac	actcacgcca	tctccaaagg	2040
cgctgctcaa	gaaagatcga	aagaaatcga	ggcgttgacc	tggtgctggt	agctattctc	2100
gaaacttgct	tctggattct	ttgccttgtg	tcgctaccga	tgcccagagt	caatccagat	2160
cttcaattcg	ctctctcaag	gccaacggga	aacaccgtgg	gttctcgctc	agattggacg	2220
agcgtactat	gagcaggcta	tgtattccga	ggcagaaaa	tacttctacc	gtgtgaagac	2280
catggcaccc	tcgcgcttgg	aagacatgga	gatctactcg	actgtccttt	ggcatctgaa	2340
gaacgatggt	gagttagcct	atgttgcgca	tgagttgatg	gaaacagacc	gcctgtcgcc	2400
acaggcgtgg	tgcgccatcg	gtaattcggt	ttcccaccag	cgagatcatg	accaggcctt	2460
gaagtgcttt	aagcgggcaa	cccagctgga	tcctcagttt	gcctacgggt	ttactcttca	2520
agggcacgag	tatgttgcca	acgaagaata	cgacaaggcg	cttgatgcat	accgtcacgg	2580
tatcagcgcg	gatagtcggc	attacaatgc	ttggtacgga	ctgggcacgg	tttatgacaa	2640
aatgggcaaa	ctggactttg	ccgaacaaca	cttcgggaat	gcggcaagca	ttaaaccgac	2700
caacgcagtt	ttgatctgct	gcattggatt	ggtactggaa	aaaatgaaca	accctaaagc	2760
ggctctcggt	caatatgggt	gcgcttggtc	cttggcacct	cattccgtac	tcgcgcgatt	2820
ccgcaaggcc	cgcgcatgga	tgaagctcca	ggagctcaaa	ttagctctgt	ctgagttgaa	2880
gattctcaaa	gacatggctc	cagacgaagc	taacgtgcat	tatctggttg	gtaagctcta	2940
caaaatgctt	cacgacaaa	ccaatgccat	taagcacttc	acaactgctt	tgaacttgga	3000
tccaaaggta	tgctatcac	ttccattccg	tcaaattacc	agacaatact	aacggattcg	3060
gttacaggca	gcacaataca	tcaaggatgc	catggaatct	cttgacgatg	acgaggagga	3120
tgatgaggac	atgagctgat	ttgcagtcca	cttcccacac	atcgatccaa	ttctggatct	3180
tacttgctac	ccccttcttc	accaggcgcc	tgctattcgg	gcttgcatct	atgagagtcg	3240
gcgttaaatt	tgatcttgga	ttttcgcagc	attagcatta	gcattataag	ggcgttttac	3300
aggcggggtt	gggttagagg	gcatttacc	ttgatcaggt	tttccaaaac	ggagctgagg	3360
ctcgtggatc	ttgtttcttg	tatattagcg	tgggttggt	ttgtcggggc	tggtcattgg	3420
ctgcatatga	gagacgaaga	cgctgaacg	acagatccat	ggacatagat	gtctgtcgaa	3480
taaggcactt	gcataatctg	cgatgtcatt	cttatgccta	ttgttatcct	tccggaaata	3540
tattccatcg	tatttgagcc	tgaaccacgg	atttactcca	gaataactta	taccactcta	3600
ctgcgcacga	ctgtagaagt	aattccagaa	gctgcaggc			3639

<210> 136

<211> 2639

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446
Genomic sequence containing the coding region

<400> 136

atgtcgccat	caatataccta	catttcaggc	cagcttaggc	agctaataata	ctatcatctc	60
gataacaatt	tgtgccgtaa	tgcgctgttc	ctcgccggtc	gtttacatgc	ttacgagccc	120
cgaacggcgg	aagcgtcgta	tttactcgct	ctctgccatc	ttcagaacgg	gcaagtcaaa	180
gccgcatacg	attacagcag	gaatttttga	tcgagaggca	cccacctcgg	ctgctcctat	240
gtcttcgcgc	aagcgtgctt	ggacctagga	aagtatctgg	aaggatcac	agcgtagag	300
cggagtaaag	gcctttgggc	ttcgaagaac	cactggagta	agtattccat	gcgctgatac	360
ttgcagtcga	cctgcattta	tttcgttgct	ttctgttact	gacacatttc	cacctgtgtc	420
tctagataag	cacagtgaga	cgcaagaca	acatctgccg	gatgcagccg	cagtattctg	480
cctgttaggt	aaattatggc	atgcgcataa	ggacatcaac	aaagctgtgg	aatgctatgt	540
tgaatctctg	aagctgaatc	ccttcatgtg	ggatgcgttc	caagggttgt	gcgacaccgg	600
taagcttttg	agaataaacc	taatacatct	agccatggct	aattgtgttc	taccgccaag	660
gagtcgaatg	ccgcgtgtca	aacatctaca	agttgaattc	tgaattgctg	gccgtattgt	720
cttcatcgcc	acaggcggat	gctgagccaa	tatccgataa	gtctgcacac	acgaatgggc	780
cactgcaagc	gcaggcgaat	gttaatccaa	gttccgatcc	ttttgcctcg	actacttctc	840
gcagtgattc	aggtaccagc	catgggagct	ctgccttgtg	ggaaaaacta	aatggaagca	900
cagtaagcgt	ggcgtcatcg	ggagtgccag	catcaatcgt	gcataagga	gccgaaacgc	960
cgagtgggtca	aagcagcgga	tctgatgagt	tccggttagc	taacggaatg	aacggcgcg	1020
atgcttcttg	ggaccctcct	ttagctcctg	caaggaaaaa	cagaacgatc	caggcaataa	1080
gcggcgagta	tccaatggac	cctcctccca	agatgaaacc	cactgggatc	cgaccaagga	1140
caaggaccag	gactgagccg	gaggaccaaa	tttcagccca	gatagaccgg	gaggcaacaa	1200
atgcgccag	ggtcggggag	cgcaaacgaa	ctgtttcttg	tcaggtagcg	catccaccga	1260
cgtcacaacc	cacagaacca	ggagcaccac	agcggcgagg	tgtgcgactc	ttcaaccaga	1320
ttaaaccac	gaccagcaaa	ttgtcggcgt	ccgcgtggg	agtcaaggat	gctagagaag	1380
tcaagaaagc	gaaagccaca	ggtacgaagg	ggcgtagcac	aaccaccacc	atgggacgag	1440
tagtgagtgg	cagccgaaaa	catgccagcg	aacatcatga	tgcagatggt	aaagacggac	1500
ggtcggtacc	gtccgcccac	actcacgcca	tctccaaagg	cgctgctcaa	gaaagatcga	1560
aagaaatcga	ggcgttgacc	tggctgctgg	agctattctc	gaaacttgct	tctggattct	1620
ttgccttgtg	tcgctaccga	tgcccagagt	caatccagat	cttcaattcg	ctctctcaag	1680
gccaacggga	aacaccgtag	gttctcgctc	agattggacg	agcgtactat	gagcaggcta	1740
tgtattccga	ggcagaaaag	tacttctacc	gtgtgaagac	catggcacc	tcgcgcttgg	1800
aagacatgga	gatctactcg	actgtccttt	ggcatctgaa	gaacgatgtt	gagttagcct	1860
atttggcgca	tgagttgatg	gaaacagacc	gcctgtcgcc	acaggcgtgg	tcgcgccatcg	1920
gtaattcggt	ttcccaccag	cgagatcatg	accaggcctt	gaagtgcctt	aagcgggcaa	1980
cccagctgga	tcctcagttt	gcctacgggt	ttactcttca	agggcacgag	tatgttgcca	2040
acgaagaata	cgacaaggcg	cttgatgcat	accgtcacgg	tatcagcgcg	gatagtcggc	2100
attacaatgc	ttggtacgga	ctgggcacgg	tttatgacaa	aatgggcaaa	ctggactttg	2160
ccgaacaaca	cttccggaat	gcggcaagca	ttaacccgac	caacgcagtt	ttgatctgct	2220
gcattggatt	ggtactggaa	aaaatgaaca	accctaaagc	ggctctcgtg	caatatggtc	2280
gcgcttggtc	cttggcacct	cattccgtac	tcgcgcgatt	ccgcaaggcc	cgcgattga	2340
tgaagctcca	ggagctcaaa	ttagctctgt	ctgagttgaa	gattctcaaa	gacatggctc	2400
cagacgaagc	taacgtgcat	tatctgttgg	gtaagctcta	caaaatgctt	cacgacaaaag	2460
ccaatgccat	taagcacttc	acaactgctt	tgaacttgga	tccaaaggta	tgccctatcac	2520
ttccattccg	tcaaattacc	agacaatact	aacggattcg	gttacaggca	gcacaataca	2580
tcaaggatgc	catggaatct	cttgacgatg	acgaggagga	tgatgaggac	atgagctga	2639

<210> 137

<211> 2430

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446

Coding region without introns

```

<400> 137
atgtcgccat caatatccta catttcaggc cagcttaggc agctaataata ctatcatctc      60
gataacaatt tgtgccgtaa tgcgctgttc ctccgccgtc gtttacatgc ttacgagccc      120
cgaacggcgg aagcgtcgta tttactcgct ctctgccatc ttcagaacgg gcaagtcaaa      180
gccgcatacg attacagcag gaatttttga tcgagaggca cccacctcgg ctgctcctat      240
gtcttcgcgc aagcgtgctt ggacctagga aagtatctgg aaggtatcac agcgttagag      300
cggagtaaaag gcctttgggc ttcgaagaac cactggaata agcacagtga gacgcgaaga      360
caacatctgc cggatgcagc cgcagtattc tgcctgttag gtaaattatg gcatgcgcat      420
aaggacatca acaaagctgt ggaatgctat gttgaatctc tgaagctgaa tcccttcatg      480
tgggatgcgt tccaagggtt gtgcgacacc ggagtcaatg tccgcgtgtc aaacatctac      540
aagttgaatt ctgaattgct ggccgtattg tcttcatcgc cacaggcgga tgctgagcca      600
atatccgata agtctgcaca cacgaatggg ccactgcaag cgcaggcgaa tgtaaatcca      660
agttccgata cttttgcctc gactacttct cgcagtgatt caggtaccag ccatgggagc      720
tctgccttgt gggaaaaaact aaatggaagc acagtaagcg tggcgctatc gggagtgcc      780
gcatcaatcg tgcataaagg agccgaaacg ccgagtgggt aaagcagcgg atctgatgag      840
ttccggttag ctaacggaat gaacggcgcg gatgcttctt gggaccctcc tttagctcct      900
gcaaggaaaa acagaacgat ccaggcaata agcggcgagt atccaatgga ccctcctccc      960
aagatgaaac ccactgggat ccgaccaagg acaaggacca ggactgagcc ggaggaccaa      1020
atctcagccc agatagaccg ggaggcaaca aatgcgccca gggtcgggga ccgcaaacga      1080
actgtttctg gtcaggttagc gcatccaccg acgtcacaac ccacagaacc aggagcaccc      1140
cagcggcgga gtgtgcgact cttcaaccag attaaacca cgaccagcaa attgtcggcg      1200
tccgcgctgg gagtcaagga tgctagagaa gtcaagaaag cgaaagccac aggtacgaag      1260
gggcgtacga caaccaccac catgggacga gtagtgagtg gcagccgaaa acatgccagc      1320
gaacatcatg atgcagatgg taaagacgga cggtcgggtac cgtccgcccc cactcacgcc      1380
atctccaaag gcgctgtcga agaaagatcg aaagaaatcg aggcgttgac ctggctgctg      1440
gagctattct cgaaacttgc ttctggattc tttgccttgt gtcgctaccg atgccagag      1500
tcaatccaga tcttcaattc gctctctcaa ggccaacggg aaacaccgtg ggttctcgt      1560
cagattggac gagcgtacta tgagcaggct atgtattccg aggcagaaaa gtacttctac      1620
cgtgtgaaga ccatggcacc ctccgcgttg gaagacatgg agatctactc gactgtcctt      1680
tggcatctga agaacgatgt tgagttagcc tatttggcgc atgagttgat ggaaacagac      1740
cgctgtcgc cacaggcggtg gtgcgccatc ggtaattcgt tttcccacca gcgagatcat      1800
gaccaggcct tgaagtgtt taagcgggca acccagctgg atcctcagtt tgcctacggg      1860
tttactcttc aagggcacga gtatgttgcc aacgaagaat acgacaaggc gcttgatgca      1920
taccgtcacg gatcagcgc ggatagtcgg cattacaatg cttgggtacgg actgggcacg      1980
gtttatgaca aaatgggcaa actggacttt gccgaacaac acttccggaa tgcggcaagc      2040
attaaccga ccaacgcagt tttgatctgc tgcattggat tggtagtgga aaaaatgaac      2100
aaccctaaag cggctctcgt gcaatatggt cgcgcttgtt ccttggcacc tcattccgta      2160
ctcgcgcgat tccgcaaggc ccgcgcattg atgaagctcc aggagctcaa attagctctg      2220
tctgagttga agattctcaa agacatggct ccagacgaag ctaacgtgca ttatctgttg      2280
ggtaagctct acaaaatgct tcacgacaaa gccaatgcca ttaagcactt cacaactgct      2340
ttgaacttgg atccaaaggc agcacaatac atcaaggatg ccatggaatc tcttgacgat      2400
gacgaggagg atgatgagga catgagctga

```

<210> 138

<211> 809

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446
Protein sequence

<400> 138

```

Met Ser Pro Ser Ile Ser Tyr Ile Ser Gly Gln Leu Arg Gln Leu Ile
1           5           10           15

```

```

Tyr Tyr His Leu Asp Asn Asn Leu Cys Arg Asn Ala Leu Phe Leu Ala
          20          25          30

```

Gly Arg Leu His Ala Tyr Glu Pro Arg Thr Ala Glu Ala Ser Tyr Leu
 35 40 45
 Leu Ala Leu Cys His Leu Gln Asn Gly Gln Val Lys Ala Ala Tyr Asp
 50 55 60
 Tyr Ser Arg Asn Phe Gly Ser Arg Gly Thr His Leu Gly Cys Ser Tyr
 65 70 75 80
 Val Phe Ala Gln Ala Cys Leu Asp Leu Gly Lys Tyr Leu Glu Gly Ile
 85 90 95
 Thr Ala Leu Glu Arg Ser Lys Gly Leu Trp Ala Ser Lys Asn His Trp
 100 105 110
 Asn Lys His Ser Glu Thr Arg Arg Gln His Leu Pro Asp Ala Ala Ala
 115 120 125
 Val Phe Cys Leu Leu Gly Lys Leu Trp His Ala His Lys Asp Ile Asn
 130 135 140
 Lys Ala Val Glu Cys Tyr Val Glu Ser Leu Lys Leu Asn Pro Phe Met
 145 150 155 160
 Trp Asp Ala Phe Gln Gly Leu Cys Asp Thr Gly Val Asn Val Arg Val
 165 170 175
 Ser Asn Ile Tyr Lys Leu Asn Ser Glu Leu Leu Ala Val Leu Ser Ser
 180 185 190
 Ser Pro Gln Ala Asp Ala Glu Pro Ile Ser Asp Lys Ser Ala His Thr
 195 200 205
 Asn Gly Pro Leu Gln Ala Gln Ala Asn Val Asn Pro Ser Ser Asp Pro
 210 215 220
 Phe Ala Ser Thr Thr Ser Arg Ser Asp Ser Gly Thr Ser His Gly Ser
 225 230 235 240
 Ser Ala Leu Trp Glu Lys Leu Asn Gly Ser Thr Val Ser Val Ala Ser
 245 250 255
 Ser Gly Val Pro Ala Ser Ile Val His Glu Gly Ala Glu Thr Pro Ser
 260 265 270
 Gly Gln Ser Ser Gly Ser Asp Glu Phe Arg Leu Ala Asn Gly Met Asn
 275 280 285
 Gly Ala Asp Ala Ser Trp Asp Pro Pro Leu Ala Pro Ala Arg Lys Asn
 290 295 300
 Arg Thr Ile Gln Ala Ile Ser Gly Glu Tyr Pro Met Asp Pro Pro Pro
 305 310 315 320
 Lys Met Lys Pro Thr Gly Ile Arg Pro Arg Thr Arg Thr Arg Thr Glu
 325 330 335
 Pro Glu Asp Gln Ile Ser Ala Gln Ile Asp Arg Glu Ala Thr Asn Ala
 340 345 350

Pro Arg Val Gly Asp Arg Lys Arg Thr Val Ser Gly Gln Val Ala His
 355 360 365
 Pro Pro Thr Ser Gln Pro Thr Glu Pro Gly Ala Pro Gln Arg Arg Ser
 370 375 380
 Val Arg Leu Phe Asn Gln Ile Lys Pro Thr Thr Ser Lys Leu Ser Ala
 385 390 395 400
 Ser Ala Leu Gly Val Lys Asp Ala Arg Glu Val Lys Lys Ala Lys Ala
 405 410 415
 Thr Gly Thr Lys Gly Arg Thr Thr Thr Thr Thr Met Gly Arg Val Val
 420 425 430
 Ser Gly Ser Arg Lys His Ala Ser Glu His His Asp Ala Asp Gly Lys
 435 440 445
 Asp Gly Arg Ser Val Pro Ser Ala His Thr His Ala Ile Ser Lys Gly
 450 455 460
 Ala Ala Gln Glu Arg Ser Lys Glu Ile Glu Ala Leu Thr Trp Leu Leu
 465 470 475 480
 Glu Leu Phe Ser Lys Leu Ala Ser Gly Phe Phe Ala Leu Cys Arg Tyr
 485 490 495
 Arg Cys Pro Glu Ser Ile Gln Ile Phe Asn Ser Leu Ser Gln Gly Gln
 500 505 510
 Arg Glu Thr Pro Trp Val Leu Ala Gln Ile Gly Arg Ala Tyr Tyr Glu
 515 520 525
 Gln Ala Met Tyr Ser Glu Ala Glu Lys Tyr Phe Tyr Arg Val Lys Thr
 530 535 540
 Met Ala Pro Ser Arg Leu Glu Asp Met Glu Ile Tyr Ser Thr Val Leu
 545 550 555 560
 Trp His Leu Lys Asn Asp Val Glu Leu Ala Tyr Leu Ala His Glu Leu
 565 570 575
 Met Glu Thr Asp Arg Leu Ser Pro Gln Ala Trp Cys Ala Ile Gly Asn
 580 585 590
 Ser Phe Ser His Gln Arg Asp His Asp Gln Ala Leu Lys Cys Phe Lys
 595 600 605
 Arg Ala Thr Gln Leu Asp Pro Gln Phe Ala Tyr Gly Phe Thr Leu Gln
 610 615 620
 Gly His Glu Tyr Val Ala Asn Glu Glu Tyr Asp Lys Ala Leu Asp Ala
 625 630 635 640
 Tyr Arg His Gly Ile Ser Ala Asp Ser Arg His Tyr Asn Ala Trp Tyr
 645 650 655
 Gly Leu Gly Thr Val Tyr Asp Lys Met Gly Lys Leu Asp Phe Ala Glu
 660 665 670
 Gln His Phe Arg Asn Ala Ala Ser Ile Asn Pro Thr Asn Ala Val Leu

675	680	685
Ile Cys Cys Ile Gly Leu Val Leu Glu Lys Met Asn Asn Pro Lys Ala		
690	695	700
Ala Leu Val Gln Tyr Gly Arg Ala Cys Ser Leu Ala Pro His Ser Val		
705	710	715
Leu Ala Arg Phe Arg Lys Ala Arg Ala Leu Met Lys Leu Gln Glu Leu		
	725	730
Lys Leu Ala Leu Ser Glu Leu Lys Ile Leu Lys Asp Met Ala Pro Asp		
	740	745
Glu Ala Asn Val His Tyr Leu Leu Gly Lys Leu Tyr Lys Met Leu His		
	755	760
Asp Lys Ala Asn Ala Ile Lys His Phe Thr Thr Ala Leu Asn Leu Asp		
	770	775
Pro Lys Ala Ala Gln Tyr Ile Lys Asp Ala Met Glu Ser Leu Asp Asp		
	785	790
Asp Glu Glu Asp Asp Glu Asp Met Ser		
	805	

<210> 139

<211> 2684

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 139

acctgttoga	cgctcacact	caaatgcgca	ccagtcgccg	cagccaaccg	gagcacatac	60
acattccacc	ggctcaatgg	ggtcgaatgg	tccacaagga	atgtccgaaa	attgggaagg	120
aagagatcaa	agacaagttc	caatgtccac	gcgtgaggta	gcaacgcccg	ggaacagacc	180
tggccttttt	gcgacctgc	acgatcgagg	gaaggtggct	aagcaaccgg	atttctatga	240
tccttacttt	ccgctcaaat	atctggagggt	accgaaatgt	acgtgagccc	tgccgtcaaa	300
ttactaccgc	ctgcttactt	gtcatggcct	ataactgacc	ctgccctgca	gccgatcata	360
tttataaaaag	agcccactac	ggtttacaat	cgggaattcc	cgatgagggtg	gactttgcat	420
tgtatcacct	tgttcagatt	tcgaatcaac	gatgggataa	attcaagttt	gaggggtttcc	480
ccttgcttgc	ggagaacctc	atggcaaagg	ccctggatat	ctcccttgtc	acaaccgggg	540
tgaagtggga	gcttcagtat	gatgttcttc	aactcagtga	tcgctgcaat	gagctgaact	600
cgctacatgg	cacacgagat	ctgttgagga	agatcaaaca	aatgccagtt	acattgccgg	660
aagacaccct	cgagacgtac	gaattcaacc	accttctgcg	caacgttaaa	gaagcgaccc	720
tggtactacg	caatatgggtc	cttctgaaag	agaatgccta	ctatgtgtca	cggtagcgga	780
aaggcctgct	ccgagacttc	ctcgtcatta	tgatcaactt	gccaatcag	cctcgtctca	840
acgagatcaa	gaacgacgct	ttggacattg	cagaggagggt	caccaagttt	atgaagaccg	900
atccggaaga	tccacttttg	atctcacttc	tcaattgtct	cgggtcgtca	gacgtgtctc	960
acgtgggtccg	cgcactctgg	gctctcacc	atctctccac	tgaattagac	gagccagagg	1020
cgaaccgggc	aatggaacgg	ataccaaaag	agactttgca	gcagctctac	tttcacactc	1080
ttctcgactt	ggacaaaagat	attctcagtg	gtgcattgga	cttctggtac	cagtatacac	1140
tttctgcccga	gaacattgag	actttgattg	aggtcttcaa	cttgccctacc	gtcttcgtcc	1200
cccggatggt	cgcactgtta	acgcacgaag	gccgaccgaa	caagaaggaa	actgtgttgc	1260
aagaagaaaa	ggtggccccc	ccaccgtcgg	atatccctcg	tgtaccgccc	gagctcatga	1320
aagagctgat	ggagcttttcg	gagcctgaac	ggagctcgcg	ttggctccgg	tgctgctttg	1380
tggaggacct	cgagtgcgag	atcacccaaa	ttgccttgtg	gcaggcgtat	cagagcagat	1440

ttgcagaccc	tcgccttccct	ggtggcggtg	ttctccctgc	ggctgaattt	atcaaaaatg	1500
tcagtagcac	tttcacgaac	gcgcaagcac	aggtgatcaa	tggccctggt	gcagccacga	1560
aattcatcat	caaaggcatt	cggccctggt	agaccgccta	taccttcgag	ggctttccct	1620
acatttactg	caagtgggcg	gacaactcga	agccaagcaa	gacgtgtcag	cgtgctttca	1680
agtcgccggc	agaacttcgc	catcacgtct	tcacggaaca	catgaacctc	aagcctactg	1740
aaacgccggg	acactataac	ctggagaagg	cggagtcgcc	cgttcatacc	tgcctttggg	1800
acaactgcac	gaaattccgg	tcgtctggtc	cgagtgccaa	tactgcaatg	gtcgctgggc	1860
acgtctccgc	acatctgccc	gaggaacgtg	cgccagatgc	ggagccgccg	acatccaaac	1920
gtgcggttct	ccaagagcgc	atcgtccgca	aatggtacta	cctggacact	ccagtcaatg	1980
agcgaggcga	gccgtttgga	gtggcctaca	aggcggcggt	agtattgcgt	aaccttgccc	2040
gaaacctgcc	tacgggtatt	gcaccgcagt	acaacgggct	ttcatggaag	aaagccgtct	2100
tccttagtca	tcgtccaaag	atcatcgaag	catgggaccg	caaccgctca	ttgcgcaagg	2160
aacttaccga	gttgatcatg	gtaatagaaa	aagaggatta	ttactgaact	tggggcgcgga	2220
gagagacgag	atgaacagta	aatgatcctc	ttcaatgacg	gctgttcggt	cttctttcaa	2280
actcacggtc	ctcgctcctta	ttcttctgca	tggccattga	tgtacaataa	tacccttttt	2340
cttccacatg	atatcttttcg	ataatctttt	cttgcttttt	cttctttcat	ttctcatgag	2400
gaactcctca	cctgaatgaa	aaggtggttg	ttttgctcct	accgttcgcc	cttcaagcta	2460
ggtgagggtt	cactcgcaat	ctaaaacaca	cggcgctctg	gtttgggggg	gtaggaatct	2520
gctgggtgat	gcacggtttc	ctttaacgat	gtactatagg	tagatcgtag	ccaggagaaa	2580
agaaaagata	ctaatacgct	aggtgctcaa	tgattccagg	tcacttggaa	aattgatcgg	2640
agcgtgagag	ctcctatcaa	ttttatccct	taagccgctt	caaa		2684

<210> 140

<211> 1707

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
Genomic sequence containing the coding region

<400> 140

atggcaaagg	ccctggatat	ctcccttgct	acaaccgggg	tgaagtggga	gcttcagtat	60
gatgttcttc	aactcagtga	tcgcgtcaat	gagctgaact	cgctacatgg	cacacgagat	120
ctgttgagga	agatcaaaca	aatgccagtt	acattggcgg	aagacaccct	cgagacgtac	180
gaattcaacc	accttctgcg	caacgttaaa	gaagcgaccc	tggtagtacg	caatatggtc	240
cttctgaaag	agaatgccta	ctatgtgtca	cggtagcgga	aaggcctgct	ccgagacttc	300
ctcgtcatta	tgatcaactt	gcccaatcag	cctcgtctca	acgagatcaa	gaacgacgct	360
ttggacattg	cagaggaggt	caccaagtgt	atgaagaccg	atccggaaga	tccacttttg	420
atctcacttc	tcaattgtct	cgggtcgtca	gatcgtgctc	acgtgggtccg	cgcactctgg	480
gctctcacc	atttctccac	tgaattagac	gagccagagc	cgaaccgggc	aatggaacgg	540
ataccaaaag	agactttgca	gcagctctac	tttcacactc	ttctcgactt	ggacaaagat	600
attctcagtg	gtgcattgga	cttctggtag	cagtatacac	tttcgtccga	gaacattgag	660
actttgattg	aggtcttcaa	cttgccctacc	cttctcgtcc	cccggatggt	cgcactgtta	720
acgcacgaag	gccgaccgaa	caagaaggaa	actgtgttgc	aagaagaaaa	ggtggccccc	780
ccaccgtcgg	atatccctcg	tgtaccgccc	gagctcatga	aagagctgat	ggagctttcg	840
gagcctgaac	ggagctcgcg	ttggctccgg	tgctgctttg	tggaggacct	cgagtgcgag	900
atcacccaaa	ttgcctttgt	gcaggcgtat	cagagcagat	ttgcagaccc	tcgccttccct	960
ggtggcggtg	ttctccctgc	ggctgaattt	atcaaaaatg	tcagtagcac	tttcacgaac	1020
gcgcaagcac	aggtgatcaa	tggccctggt	gcagccacga	aattcatcat	caaaggcatt	1080
cggccctggt	agaccgccta	taccttcgag	ggctttccct	acatttactg	caagtgggcg	1140
gacaactcga	agccaagcaa	gacgtgtcag	cgtgctttca	agtcgccggc	agaacttcgc	1200
catcacgtct	tcacggaaca	catgaacctc	agccctactg	aaacgccggg	acactataac	1260
ctggagaagg	cggagtgcgc	cgttcatacc	tgccctttgg	acaactgcac	gaaattccgg	1320
tcgtctggtc	cgagtgccaa	tactgcaatg	gtcgctgggc	acgtctccgc	acatctgccc	1380
gaggaacgtg	cgccagatgc	ggagccggcg	acatccaaac	gtgcggttct	ccaagagcgc	1440
atcgtccgca	aatggtacta	cctggacact	ccagtcaatg	agcgaggcga	gccgtttgga	1500
gtggcctaca	aggcggcggt	agtattgcgt	aaccttgccc	gaaacctgcc	tacgggtatt	1560
gcaccgcagt	acaacgggct	ttcatggaag	aaagccgtct	tccttagtca	tcgtccaaag	1620
atcatcgaag	catgggaccg	caaccgctca	ttgcgcaagg	aacttaccga	gttgatcatg	1680

gtaatagaaa aagaggatta ttactga

1707

<210> 141

<211> 1707

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
Coding region without introns

<400> 141

atggcaaagg	ccctggatat	ctcccttgtc	acaaccgggg	tgaagtggga	gcttcagtat	60
gatgttcttc	aactcagtga	tcgcgtcaat	gagctgaact	cgctacatgg	cacacgagat	120
ctgttgagg	agatcaaaca	aatgccagtt	acattgccgg	aagacaccct	cgagacgtac	180
gaattcaacc	accttctgcg	caacgttaaa	gaagcgaccc	tggtactacg	caatatggtc	240
cttctgaaag	agaatgccta	ctatgtgtca	cggtacgcga	aaggcctgct	ccgagacttc	300
ctcgtcatta	tgatcaactt	gcccaatcag	cctcgtctca	acgagatcaa	gaacgacgct	360
ttggacattg	cagaggaggt	caccaagttt	atgaagaccg	atccggaaga	tccacttttg	420
atctcacttc	tcaattgtct	cgggtcgctc	gatcgtgctc	acgtgggccg	cgcactctgg	480
gctctcacc	atttctccac	tgaattagac	gagccagagg	cgaaccgggc	aatggaacgg	540
ataccaaaag	agactttgca	gcagctctac	tttcacactc	ttctcgactt	ggacaaagat	600
attctcagtg	gtgcattgga	cttctgggtac	cagtatacac	tttcgtccga	gaacattgag	660
actttgattg	aggtcttcaa	cttgccctacc	gtcttcgtcc	cccggatggt	cgcactgtta	720
acgcacgaag	gccgaccgaa	caagaaggaa	actgtgttgc	aagaagaaaa	ggtggccccc	780
ccaccgtcgg	atatccctcg	tgtaccgccc	gagctcatga	aagagctgat	ggagctttcg	840
gagcctgaac	ggagctcgcg	ttggctccgg	tgctgctttg	tggaggacct	cgagtgcgag	900
atcacccaaa	ttgccttggtg	gcaggcgtat	cagagcagat	ttgcagaccc	tcgccttcct	960
ggtggcggtg	ttctccctgc	ggctgaattt	atcaaaaatg	tcagtacgac	tttcacgaac	1020
gcgcaagcac	aggtgatcaa	tggccctggt	gcagccacga	aattcatcat	caaaggcatt	1080
cggccccctg	agaccgccta	taccttcgag	ggctttccct	acatttactg	caagtgggcg	1140
gacaactcga	agccaagcaa	gacgtgtcag	cgtgctttca	agtcgccggc	agaacttcgc	1200
catcacgtct	tcacggaaca	catgaacctc	aagcctactg	aaacgccggg	acactataac	1260
ctggagaagg	cggagtcgcc	cgttcatacc	tgccctttgg	acaactgcac	gaaattccgg	1320
tcgtctggtc	cgagtgccaa	tactgcaatg	gtcgtggtgg	acgtctccgc	acatctgccc	1380
gaggaacgtg	cgccagatgc	ggagccgccc	acatccaaac	gtgcggttct	ccaagagcgc	1440
atcgctcgca	aatggtacta	cctggacact	ccagtcaatg	agcgaggcga	gccgtttgga	1500
gtggcctaca	aggcggcggt	agtattgcgt	aaccttgccc	gaaacctgcc	tacgggtatt	1560
gcaccgcagt	acaacgggct	ttcatggaag	aaagccgtct	tccttagtca	tcgtccaaag	1620
atcatcgaag	catgggaccg	caaccgctca	ttgcgcgaag	aacttaccga	gttgatcatg	1680
gtaatagaaa	aagaggatta	ttactga				1707

<210> 142

<211> 568

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
Protein sequence

<400> 142

Met	Ala	Lys	Ala	Leu	Asp	Ile	Ser	Leu	Val	Thr	Thr	Gly	Val	Lys	Trp
1				5					10					15	

Glu	Leu	Gln	Tyr	Asp	Val	Leu	Gln	Leu	Ser	Asp	Arg	Val	Asn	Glu	Leu
		20						25					30		

Asn Ser Leu His Gly Thr Arg Asp Leu Leu Glu Lys Ile Lys Gln Met
 35 40 45
 Pro Val Thr Leu Pro Glu Asp Thr Leu Glu Thr Tyr Glu Phe Asn His
 50 55 60
 Leu Leu Arg Asn Val Lys Glu Ala Thr Leu Val Leu Arg Asn Met Val
 65 70 75 80
 Leu Leu Lys Glu Asn Ala Tyr Tyr Val Ser Arg Tyr Ala Lys Gly Leu
 85 90 95
 Leu Arg Asp Phe Leu Val Ile Met Ile Asn Leu Pro Asn Gln Pro Arg
 100 105 110
 Leu Asn Glu Ile Lys Asn Asp Ala Leu Asp Ile Ala Glu Glu Val Thr
 115 120 125
 Lys Phe Met Lys Thr Asp Pro Glu Asp Pro Leu Trp Ile Ser Leu Leu
 130 135 140
 Asn Cys Leu Gly Ser Ser Asp Arg Ala His Val Val Arg Ala Leu Trp
 145 150 155 160
 Ala Leu Thr His Phe Ser Thr Glu Leu Asp Glu Pro Glu Ala Asn Arg
 165 170 175
 Ala Met Glu Arg Ile Pro Lys Glu Thr Leu Gln Gln Leu Tyr Phe His
 180 185 190
 Thr Leu Leu Asp Leu Asp Lys Asp Ile Leu Ser Gly Ala Leu Asp Phe
 195 200 205
 Trp Tyr Gln Tyr Thr Leu Ser Ser Glu Asn Ile Glu Thr Leu Ile Glu
 210 215 220
 Val Phe Asn Leu Pro Thr Val Phe Val Pro Arg Met Val Ala Leu Leu
 225 230 235 240
 Thr His Glu Gly Arg Pro Asn Lys Lys Glu Thr Val Leu Gln Glu Glu
 245 250 255
 Lys Val Ala Pro Pro Pro Ser Asp Ile Pro Arg Val Pro Pro Glu Leu
 260 265 270
 Met Lys Glu Leu Met Glu Leu Ser Glu Pro Glu Arg Ser Ser Arg Trp
 275 280 285
 Leu Arg Cys Cys Phe Val Glu Asp Leu Glu Cys Glu Ile Thr Gln Ile
 290 295 300
 Ala Leu Trp Gln Ala Tyr Gln Ser Arg Phe Ala Asp Pro Arg Leu Pro
 305 310 315 320
 Gly Gly Gly Val Leu Pro Ala Ala Glu Phe Ile Lys Asn Val Ser Thr
 325 330 335
 Thr Phe Thr Asn Ala Gln Ala Gln Val Ile Asn Gly Pro Gly Ala Ala
 340 345 350

Thr Lys Phe Ile Ile Lys Gly Ile Arg Pro Leu Glu Thr Ala Tyr Thr
 355 360 365
 Phe Glu Gly Phe Pro Tyr Ile Tyr Cys Lys Trp Ala Asp Asn Ser Lys
 370 375 380
 Pro Ser Lys Thr Cys Gln Arg Ala Phe Lys Ser Pro Ala Glu Leu Arg
 385 390 395 400
 His His Val Phe Thr Glu His Met Asn Leu Lys Pro Thr Glu Thr Pro
 405 410 415
 Gly His Tyr Asn Leu Glu Lys Ala Glu Ser Pro Val His Thr Cys Leu
 420 425 430
 Trp Asp Asn Cys Thr Lys Phe Arg Ser Ser Gly Pro Ser Ala Asn Thr
 435 440 445
 Ala Met Val Ala Gly His Val Ser Ala His Leu Pro Glu Glu Arg Ala
 450 455 460
 Pro Asp Ala Glu Pro Pro Thr Ser Lys Arg Ala Val Leu Gln Glu Arg
 465 470 475 480
 Ile Val Arg Lys Trp Tyr Tyr Leu Asp Thr Pro Val Asn Glu Arg Gly
 485 490 495
 Glu Pro Phe Gly Val Ala Tyr Lys Ala Ala Leu Val Leu Arg Asn Leu
 500 505 510
 Ala Arg Asn Leu Pro Thr Gly Ile Ala Pro Gln Tyr Asn Gly Leu Ser
 515 520 525
 Trp Lys Lys Ala Val Phe Leu Ser His Arg Pro Lys Ile Ile Glu Ala
 530 535 540
 Trp Asp Arg Asn Arg Ser Leu Arg Lys Glu Leu Thr Glu Leu Ile Met
 545 550 555 560
 Val Ile Glu Lys Glu Asp Tyr Tyr
 565

<210> 143

<211> 2542

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 143

aggcacacag	tgcactgtac	tgactcagtt	gttcctccag	gcctcgataa	cacgacttac	60
gtctagtgtc	atctccttcc	acgtttccaa	ttatcttctc	ttttccttcc	aaaaaaatta	120
aaaagcagat	actctcgtct	gctagaccgc	atactttgac	cggtatcggt	atcttccagt	180
acgagggtgc	tcggcatata	gtcacaattc	ctttttcaag	aggctttttc	ctcctctccc	240
tatcctttcg	ccctccctag	catccctttc	gagcttgcc	taatttcgtc	catctggcct	300
gtgtgccatt	ctcttcattg	cgatcaagg	ccttctctct	caggcggaca	cagccccctt	360
gttcgtctgg	gcagcagata	gtgcttcc	ggcttctgtg	tctacggtca	actacatata	420
caccactgcg	ttgctcctca	tctcaataat	cggctcttgca	ccagcatacg	tcacacaatt	480

cattacgtca	atcagcggaa	atggtctaca	tccgcatccc	caagaactac	acggcttcgc	540
cgtcttcctt	tgccggaact	ccgtccttga	cgatcaatta	cgaggcaacg	caggatcttg	600
attctacca	tgcttttgaa	ggtttgttga	cgccggtgac	acgtgtgaga	gcagcgctgg	660
acagaggctg	acagtctaca	ggccagaga	aactcttgga	ggtgtggttc	gcgccttccg	720
ctcaggaatt	aggtccagcg	cagcccgcg	gtctgaaggc	tgttccggag	gagatctgga	780
aggacatgtt	ggatctcgtc	aattgccagg	tcctctcgat	tgtttcgtca	gaggatgtgg	840
acgcctacct	gctctccgag	tctagcatgt	tcgtttggcc	tcacaaactc	atcttgaaga	900
cttgtggtac	caccactctt	ctgtctggtc	tcccacgc	tctcgagatt	gccgctttgt	960
tcggtggctt	ccccaaagtct	accgcccctt	ctcgcggaat	ctccgtcgcc	gctgcgccct	1020
accgcttctt	ctacagccgc	aagaacttcc	tgttccccga	ccgccagcgg	ggccctcacc	1080
gcagctggag	agatgaagtg	cggactatgg	ataagctctt	cctcaacggc	agcgcctaca	1140
tgattggcaa	gatgaatggc	gagcactgg	acttgtacct	gactgaacct	cataccatgc	1200
tcaccccgcc	aacgagcccg	ggagccaaga	ccgagtttac	ggaaacggag	accaaggtcc	1260
tcagtgtacc	ccagggcgct	gctctgcaga	ctgattcgga	ggatgagact	ttggaagtct	1320
tgatgaccga	cttggatgag	gagaacgcca	agcagttcta	cctcgagaat	gccactgccg	1380
ttgctggagaa	ccgttatcgc	aactcaaatt	cggagaagag	tggccatgtt	gatgttttca	1440
gcaacacttc	ctccgatata	agcgattttg	actccgacgg	aagccaggtt	ctgcctccag	1500
agttgactac	cgagggtcac	gcgctcgga	ccgtggtctc	tgaagcctgt	ggactttcct	1560
ctgtgtatcc	taaggagaag	tatcccgtat	cgcgcacga	tgcctacctg	tttacaccat	1620
gcggcttctc	cgccaacggc	gtgattccgc	ctcctgagg	aaaagctgga	acccactact	1680
tcacagtaca	cgctactcca	gagccgcact	gttcatatgc	gtcctttgag	accaacgtac	1740
cgcaactcga	gaacggccag	actaccgctg	gaatcatcaa	gcaagtggc	gacatcttca	1800
agcctggctg	cttcagcgtg	actctcttcg	aggccaagcc	agcgtgagc	caggtcgaag	1860
acgagtggaa	ggaagccaag	tacctggccg	ctcgtcggac	cgccaaaatg	gaacatgtgg	1920
agggatatcg	ccgagtggac	cggattgtcc	acgacctcga	cggctatgag	cttgtcttcc	1980
gctattatga	acgcctggac	tggaaagggg	gggcccctcg	gctgggagag	gagagatctt	2040
gaagaacagg	ccatagcacg	ttgagataat	cttttgcttg	cggaatttgg	ttggacattc	2100
ttttgagatg	gaaatggttt	cattctgcac	tttttctacg	tctgccaat	attcgctgaa	2160
cagccctgtg	ctcacttcat	ttgagctcgc	agagtatcct	tcgacaacat	gagcgttcgt	2220
ttcgtgtaca	aagctcattg	actccctgta	ctgtcgttac	tgttctgatt	ttgcattgag	2280
ctacccgagc	gtttgcagtg	atcatgtgat	tatatgattc	gtattcatac	gttctttcag	2340
tcgtatgcga	atatttttta	taacatatat	ctaggatatg	tatccaagtt	caagaaggta	2400
gactcgtagt	agaatgtgtt	gatccagttg	atggccgacg	ccaactggta	tcgattacgg	2460
attggcagac	gtgccagatc	agtcggaggt	ttcttttttg	ttgggatcgc	atcacagctc	2520
caacacgaca	ttcaactttc	aa				2542

<210> 144

<211> 1542

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101
Genomic sequence containing the coding region

<400> 144

atggtctaca	tccgcatccc	caagaactac	acggcttcgc	cgtcttcctt	tgccggaact	60
ccgtccttga	cgatcaatta	cgaggcaacg	caggatcttg	attctacca	tgcttttgaa	120
ggtttgttga	cgccggtgac	acgtgtgaga	gcagcgctgg	acagaggctg	acagtctaca	180
ggccagaga	aactcttgga	ggtgtggttc	gcgccttccg	ctcaggaatt	aggtccagcg	240
cagcccgcg	gtctgaaggc	tgttccggag	gagatctgga	aggacatgtt	ggatctcgtc	300
aattgccagg	tcctctcgat	tgtttcgtca	gaggatgtgg	acgcctacct	gctctccgag	360
tctagcatgt	tcggtttggc	tcacaaactc	atcttgaaga	cttgtggtac	caccactctt	420
ctgtctggtc	tcccacgc	tctcgagatt	gccgctttgt	tcggtggctt	ccccaaagtct	480
accgcccctt	ctcgcggaat	ctccgtcgcc	gctgcgccct	accgcttctt	ctacagccgc	540
aagaacttcc	tgttccccga	ccgccagcgg	ggccctcacc	gcagctggag	agatgaagtg	600
cggactatgg	ataagctctt	cctcaacggc	agcgcctaca	tgattggcaa	gatgaatggc	660
gagcactgg	acttgtacct	gactgaacct	cataccatgc	tcaccccgcc	aacgagcccg	720
ggagccaaga	ccgagtttac	ggaaacggag	accaaggtcc	tcagtgtacc	ccagggcgct	780
gctctgcaga	ctgattcggga	ggatgagact	ttggaagtct	tgatgaccga	cttggatgag	840

gagaacgcc	agcagttcta	cctcgagaat	gccactgccg	ttgcggagaa	ccgttatcgc	900
aactcaaatt	cggagaagag	tggccatggt	gatgttttca	gcaacacttc	ctccgatatc	960
agcgattttg	actccgacgg	aagccagggt	ctgcctccag	agttgactac	cgagggtcac	1020
gcgctcgaa	ccgtggtctc	tgaagcctgt	ggactttcct	ctgtgtatcc	taaggagaag	1080
tatcccgatt	cgcgcatcga	tgcctacctg	tttacaccat	gcggcttctc	cgccaacggc	1140
gtgattccgc	ctcctgaggg	aaaagctgga	acccactact	tcacagtaca	cgtcactcca	1200
gagccgcact	gttcatatgc	gtcctttgag	accaacgtac	cgactcgcga	gaacggccag	1260
actaccgctg	gaatcatcaa	gcaagtgggc	gacatcttca	agcctggtcg	cttcagcgtg	1320
actctcttcg	aggccaagcc	agcgtcgagc	caggtcgaag	acgagtggaa	ggaagccaag	1380
tacctggccg	ctcgtcggac	cgccaaaatg	gaacatgtgg	agggatatcg	ccgagtggac	1440
cggattgtcc	acgacctcga	cggctatgag	cttgtcttcc	gctattatga	acgcctggac	1500
tggaaagggg	gggcccctcg	gctgggagag	gagagatctt	ga		1542

<210> 145

<211> 1482

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101
Coding region without introns

<400> 145

atggtctaca	tcggcattccc	caagaactac	acggcttcgc	cgctcttcctt	tgccggaact	60
ccgtcccttga	cgatcaatta	cgaggcaacg	caggatcttg	attctacca	tgcttttgaa	120
ggtccagaga	aactcttgga	ggtgtggttc	gcgccttcgc	ctcaggaatt	aggtccagcg	180
cagcccgcgc	gtctgaaggc	tggtccggag	gagatctgga	aggacatggt	ggatctcgtc	240
aattgccagg	tcctctcgat	tgtttcgtca	gaggatgtgg	acgcctacct	gctctccgag	300
tctagcatgt	tcgtttggcc	tcacaaactc	atcttgaaga	cttgtggtac	caccactctt	360
ctgtctggtc	tcccacgcat	tctcgagatt	gccgctttgt	tcgggtggctt	cccccaagtct	420
accgcccctt	ctcgcggaat	ctccgtcgcc	gctgcgcctt	accgcgtctt	ctacagccgc	480
aagaacttcc	tggtccccga	ccgccagcgg	ggccctcacc	gcagctggag	agatgaagtg	540
cggactatgg	ataagctctt	cctcaacggc	agcgcctaca	tgattggcaa	gatgaatggc	600
gagcactggt	acttgtacct	gactgaacct	cataccatgc	tcaccccgcg	aacgagcccg	660
ggagccaaga	ccgagtttac	ggaaacggag	accaagggtc	tcagtgtacc	ccagggcgct	720
gctctgcaga	ctgattcgga	ggatgagact	ttggaagtct	tgatgaccga	cttggatgag	780
gagaacgcc	agcagttcta	cctcgagaat	gccactgccg	ttgcggagaa	ccgttatcgc	840
aactcaaatt	cggagaagag	tggccatggt	gatgttttca	gcaacacttc	ctccgatatc	900
agcgattttg	actccgacgg	aagccagggt	ctgcctccag	agttgactac	cgagggtcac	960
gcgctcggaa	ccgtggtctc	tgaagcctgt	ggactttcct	ctgtgtatcc	taaggagaag	1020
tatcccgatt	cgcgcatcga	tgcctacctg	tttacaccat	gcggcttctc	cgccaacggc	1080
gtgattccgc	ctcctgaggg	aaaagctgga	acccactact	tcacagtaca	cgtcactcca	1140
gagccgcact	gttcatatgc	gtcctttgag	accaacgtac	cgactcgcga	gaacggccag	1200
actaccgctg	gaatcatcaa	gcaagtgggc	gacatcttca	agcctggtcg	cttcagcgtg	1260
actctcttcg	aggccaagcc	agcgtcgagc	caggtcgaag	acgagtggaa	ggaagccaag	1320
tacctggccg	ctcgtcggac	cgccaaaatg	gaacatgtgg	agggatatcg	ccgagtggac	1380
cggattgtcc	acgacctcga	cggctatgag	cttgtcttcc	gctattatga	acgcctggac	1440
tggaaagggg	gggcccctcg	gctgggagag	gagagatctt	ga		1482

<210> 146

<211> 493

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101
Protein sequence

<400> 146

Met Val Tyr Ile Gly Ile Pro Lys Asn Tyr Thr Ala Ser Pro Ser Ser
 1 5 10 15
 Phe Ala Gly Thr Pro Ser Leu Thr Ile Asn Tyr Glu Ala Thr Gln Asp
 20 25 30
 Leu Asp Ser Thr Asn Ala Phe Glu Gly Pro Glu Lys Leu Leu Glu Val
 35 40 45
 Trp Phe Ala Pro Ser Ala Gln Glu Leu Gly Pro Ala Gln Pro Ala Gly
 50 55 60
 Leu Lys Ala Val Pro Glu Glu Ile Trp Lys Asp Met Leu Asp Leu Val
 65 70 75 80
 Asn Cys Gln Val Leu Ser Ile Val Ser Ser Glu Asp Val Asp Ala Tyr
 85 90 95
 Leu Leu Ser Glu Ser Ser Met Phe Val Trp Pro His Lys Leu Ile Leu
 100 105 110
 Lys Thr Cys Gly Thr Thr Thr Leu Leu Ser Gly Leu Pro Arg Ile Leu
 115 120 125
 Glu Ile Ala Ala Leu Phe Gly Gly Phe Pro Lys Ser Thr Ala Pro Ser
 130 135 140
 Arg Gly Ile Ser Val Ala Ala Ala Pro Tyr Arg Val Phe Tyr Ser Arg
 145 150 155 160
 Lys Asn Phe Leu Phe Pro Asp Arg Gln Arg Gly Pro His Arg Ser Trp
 165 170 175
 Arg Asp Glu Val Arg Thr Met Asp Lys Leu Phe Leu Asn Gly Ser Ala
 180 185 190
 Tyr Met Ile Gly Lys Met Asn Gly Glu His Trp Tyr Leu Tyr Leu Thr
 195 200 205
 Glu Pro His Thr Met Leu Thr Pro Pro Thr Ser Pro Gly Ala Lys Thr
 210 215 220
 Glu Phe Thr Glu Thr Glu Thr Lys Val Leu Ser Val Pro Gln Gly Ala
 225 230 235 240
 Ala Leu Gln Thr Asp Ser Glu Asp Glu Thr Leu Glu Val Leu Met Thr
 245 250 255
 Asp Leu Asp Glu Glu Asn Ala Lys Gln Phe Tyr Leu Glu Asn Ala Thr
 260 265 270
 Ala Val Ala Glu Asn Arg Tyr Arg Asn Ser Asn Ser Glu Lys Ser Gly
 275 280 285
 His Val Asp Val Phe Ser Asn Thr Ser Ser Asp Ile Ser Asp Phe Asp
 290 295 300
 Ser Asp Gly Ser Gln Val Leu Pro Pro Glu Leu Thr Thr Glu Gly His
 305 310 315 320

Ala Leu Gly Thr Val Val Ser Glu Ala Cys Gly Leu Ser Ser Val Tyr
 325 330 335

Pro Lys Glu Lys Tyr Pro Asp Ser Arg Ile Asp Ala Tyr Leu Phe Thr
 340 345 350

Pro Cys Gly Phe Ser Ala Asn Gly Val Ile Pro Pro Pro Glu Gly Lys
 355 360 365

Ala Gly Thr His Tyr Phe Thr Val His Val Thr Pro Glu Pro His Cys
 370 375 380

Ser Tyr Ala Ser Phe Glu Thr Asn Val Pro His Ser Gln Asn Gly Gln
 385 390 395 400

Thr Thr Ala Gly Ile Ile Lys Gln Val Val Asp Ile Phe Lys Pro Gly
 405 410 415

Arg Phe Ser Val Thr Leu Phe Glu Ala Lys Pro Ala Leu Ser Gln Val
 420 425 430

Glu Asp Glu Trp Lys Glu Ala Lys Tyr Leu Ala Ala Arg Arg Thr Ala
 435 440 445

Lys Met Glu His Val Glu Gly Tyr Arg Arg Val Asp Arg Ile Val His
 450 455 460

Asp Leu Asp Gly Tyr Glu Leu Val Phe Arg Tyr Tyr Glu Arg Leu Asp
 465 470 475 480

Trp Lys Gly Gly Ala Pro Arg Leu Gly Glu Glu Arg Ser
 485 490

<210> 147

<211> 1637

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 147

aaagatagag	aagacgttgc	gcggaacctt	ttgaggaccc	tcagctctat	ttgagtgtct	60
gtcacgaggt	ccatatctgg	cgatacggag	ggctggctgt	acaattaggt	tactcttatt	120
tcctactgat	ctagtgatat	aaagtttgga	tgcattatgt	aaattaaatc	tcgggggcaa	180
atgaacattt	cgaatatcgt	tataaaactc	acagaaagtg	ctgtcaatgg	cacaaattta	240
gcaatcaata	ctcatctgag	tatgttggtg	ataagtccga	aaacaaccta	aatattttacc	300
tcattaggaa	aggtgcactc	cgtagttacc	tcgactcgcg	gttagtctgg	tgactaagtt	360
cttggcgttg	tgatgagggc	aagtcctatc	atgtgatcat	agttagggtt	tccacacacc	420
aggctctcca	atatagcaag	aaaatagaag	gattagggtc	cgtctccgaa	catccatccc	480
gccagcacac	aaccgcctaaa	atgggtcgcg	ttagaaccaa	ggtaagttac	agatgaagca	540
tcatgagtta	tcttcaaaaa	agccccaaga	gagtatcatt	tctgacgaaa	tgggtttttc	600
ttcaatagac	agtcaagagg	tccgccaagg	tcatcatcga	gcgctactac	cccaagttga	660
cgctcgactt	tgagaccaac	aagcgtcttt	gcgatgagat	cgctatcatt	gcctccaagc	720
gccttcgcaa	caaggtgggc	aatccatcac	tgagccgtac	aacagtcgga	atttgacttg	780
ctgacgaaaa	ctagattgct	ggttacacca	cccaccttat	gaagcgtatc	cagcgtggcc	840
ctgtccgcgg	tatctctttc	aagctgcagg	aggaggagcg	tgagcgcaag	gatcagtagc	900
ttcctgaggt	ttccgctctg	gatgtttccc	agaccgagtc	cggccagctc	gatgtcagtg	960
ccgacaccaa	ggaccttctc	aagtccatgg	gcgtaagttc	tggttctcaac	gcggttggtc	1020

gtgggttttaa	agcagtcctgt	taacttatat	tgcccactac	agttcgacaa	tctcaaggtc	1080
aacgttgtca	acgtctccca	acatcagggt	caggagcgcc	cccgccgctt	ccggtagatg	1140
cgcgaccccc	tcgagcctcg	aaaaaaaaag	taccgattgt	cttcggtcga	tctatggcgt	1200
gctcaatcac	acttgctctg	gctgacttcg	cagctatgat	gtagcctaga	gacacaggaa	1260
tgaacataat	tctctctgag	aaagggtgctg	ctgattctcc	tggtggagat	gacgcttgat	1320
tgccaaaatt	tctccttttg	cttactgtcc	gtttcagctc	gggcgctgcg	tagaagggtc	1380
tctctgcatg	atgcgagga	tgatcatcaga	gagtcgaaac	ctttggtgcg	aactgcacca	1440
tcaactgcac	cgcattggat	cagatccata	ttaatcagtc	tatctacaga	agtaaattgg	1500
gtatcgtcat	aagcacaag	acgccgtaga	accacaaatc	gaaccacccc	atcgaattct	1560
gtcgtgacca	ggctcacgcc	aaacccgctg	agattgaagc	atatcatgat	cagatttcct	1620
ttggcacgta	gccttca					1637

<210> 148

<211> 637

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827
Genomic sequence containing the coding region

<400> 148

atggggtcgcg	ttagaaccaa	ggtaagttac	agatgaagca	tcatgagtta	tcttcaaaaa	60
agcccaaaaa	gagtatcatt	tctgacgaaa	tgggtttttc	ttcaatagac	agtcaagagg	120
tccgccaaag	tcatcatcga	gcgctactac	cccaagttga	cgctcgactt	tgagaccaac	180
aagcgtcttt	gcgatgagat	cgctatcatt	gcctccaagc	gccttcgcaa	caagggtgggc	240
aatccatcac	tgagccgtac	aacagtcgga	atttgacttg	ctgacgaaaa	ctagattgct	300
ggttacacca	cccaccttat	gaagcgtatc	cagcgtggcc	ctgtccgcgg	tatctctttc	360
aagctgcagg	aggaggagcg	tgagcgcaag	gatcagtag	ttcctgaggt	ttccgctctg	420
gatgtttccc	agaccgagtc	cggccagctc	gatgtcgatg	ccgacaccaa	ggaccttctc	480
aagtccatgg	gcgtaagttc	tgttctcaac	gcggttggtc	gtgggtttta	agcagtcctg	540
taacttatat	tgcccactac	agttcgacaa	tctcaaggtc	aacgttgta	acgtctccca	600
acatcagggt	caggagcgcc	cccgccgctt	ccggtag			637

<210> 149

<211> 420

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827
Coding region without introns

<400> 149

atggggtcgcg	ttagaaccaa	gacagtcaag	agggtccgcca	aggatcatcat	cgagcgctac	60
taccccaagt	tgacgctcga	ctttgagacc	aacaagcgtc	tttgcgatga	gatcgctatc	120
attgcctcca	agcgccttcg	caacaagatt	gctgggttaca	ccacccacct	tatgaagcgt	180
atccagcgtg	gccctgtccg	cggtatctct	ttcaagctgc	aggaggagga	gcgtgagcgc	240
aaggatcagt	acgttcctga	ggtttcgcgt	ctggatgttt	cccagaccga	gtccggccag	300
ctcgatgtcg	atgccgacac	caaggacctt	ctcaagtcca	tgggcttcga	caatctcaag	360
gtcaacgttg	tcaacgtctc	ccaacatcag	gttcaggagc	gccccgcgg	cttcgggtag	420

<210> 150

<211> 139

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827

Protein sequence

<400> 150

```

Met Gly Arg Val Arg Thr Lys Thr Val Lys Arg Ser Ala Lys Val Ile
 1              5              10              15

Ile Glu Arg Tyr Tyr Pro Lys Leu Thr Leu Asp Phe Glu Thr Asn Lys
      20              25              30

Arg Leu Cys Asp Glu Ile Ala Ile Ile Ala Ser Lys Arg Leu Arg Asn
      35              40              45

Lys Ile Ala Gly Tyr Thr Thr His Leu Met Lys Arg Ile Gln Arg Gly
      50              55              60

Pro Val Arg Gly Ile Ser Phe Lys Leu Gln Glu Glu Arg Glu Arg
      65              70              75              80

Lys Asp Gln Tyr Val Pro Glu Val Ser Ala Leu Asp Val Ser Gln Thr
      85              90              95

Glu Ser Gly Gln Leu Asp Val Asp Ala Asp Thr Lys Asp Leu Leu Lys
      100              105              110

Ser Met Gly Phe Asp Asn Leu Lys Val Asn Val Val Asn Val Ser Gln
      115              120              125

His Gln Val Gln Glu Arg Pro Arg Arg Phe Arg
      130              135

```

<210> 151

<211> 2037

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA262; clone 10-2-18

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 151

```

aaggtagtag gtgcagatat tgttgataga catttcaaaa tgtattagtt acatgattac      60
ttacttagat gtaatctttc gataataact tctagtcttg ttgagttcag aaggccagtg      120
tgtgctgaaa atgacagcga cctatgcggt gcccgtagtag cgaagagcac tggctggaaa      180
taagaagttt attagaggag cctcatgatg cataatcatt gtaagcgcac gatgcacaat      240
aatatatccg aatttctcca gatgacacta agataataac gaaaatatca catgacgttg      300
tgggcaggta tgtattatgt aatctgatcg gtagggccga tgtctcgctt agcggacttt      360
tctgtgggat tgcaatttca acttattatt ccgccgacca gcaacaaagc ggttactcga      420
ctcgactccc tccaccagag cccgtggtgt gatatacctg tctgtctttg atcctcgcaa      480
gatagacttg agtcgcagtt atggcggttg gaaagtatgc caattcactt ctattattgt      540
tctgaacgct ttttagcatgt gtctggatac ggtggtttac aggtactgat ccgggaacag      600
gaacaagcgc ttgtcgaagg gcaagaaggg tgtaagaagg aggaccgttg atcctttctc      660
caggaaggac gaataactctg ttaaggtagt tcgacgtgga ctgtgtaagt cgaccgcagc      720
taatctatat caggcgctt ccactttcca gatcagagag tatgttgcac gcatatgatg      780
tcgaattgca ggataaaggc gattcacaat ggtagtgag attatgctga ctgaattata      840
gtgtcgggaa gactctggtc aaccgcacca gtggtctcaa gaacgccaat gactccctga      900
agggtcgaat tttcagagtc tcgctggctg acctgcagaa tgatgaagac catgctttcc      960
gcaagggttaa gcttcgtgtg gacgaggttc agggcaagaa ctgtttgacc aacttccacg      1020
gtcttgattt cacaaccgac aaattgcgat ccctcgtagc caagtggcag tcgctgatcg      1080
aagccaatgt cactgtgaag acgaccgatg attatctcct tcggcttttt gctatcgctt      1140

```

tcaccaagag	acgcccgaac	cagattaaga	agaccacata	tgctcggttct	tctcaaatacc	1200
gtgccatccg	caagaagatg	attgaaatca	tgagagggga	ggcagccagc	tgctctctcg	1260
ctcagctcac	tcacaagctc	attcctgagg	tcattgggtcg	tgagatcgag	aaggctaccc	1320
agggaatcta	tcctttgcag	aatgtgtgtg	accctgttat	tcttactcgg	gatgaagact	1380
aactgcaatc	taggtccata	ttcgcaaggt	caagcttctt	aaggctccca	agttcgacct	1440
gggtgcactg	ctgaatctgc	acggtgaatc	tacaaccgat	gataagggcc	acaaggtcga	1500
gagagagttc	aaggagcagg	ttctcgaaag	cgtttaagtg	gactgaatta	ccagtatgct	1560
ggttattcgg	gacattgatt	tgtacctacc	tgtatgcttg	gattcttttt	ttatgagtta	1620
aaatgggaaa	agaacttttg	tcgcggcatc	atgtctttat	tgactgggtg	tgctcgtaac	1680
ttctatgtcc	tttgagaatg	gagcttgcaa	agaaaacttt	gcccttattc	aaatatttaa	1740
ttggacaatt	ccgatcaaa	tttagcagta	gaataacctgc	tataccagtg	atgtgctgat	1800
gcaacgggca	cctgcagttt	actttcagtt	gattcaaatt	ctatattaac	agagcccttt	1860
taccacacca	ctgacctggg	attagtatag	tgtctcgccc	taggagacta	aagaattgct	1920
agaagtatgg	ttatacataa	tgttgaatag	ttagtagtat	ttattaatat	tattttcagt	1980
gcactgatat	atatcataat	gctactaaat	atagctaccc	taagatttat	atagaga	2037

<210> 152

<211> 1037

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA262; clone 10-2-18

Genomic sequence containing the coding region

<400> 152

atggcggttg	gaaagtatgc	caattcactt	ctattattgt	tctgaacgct	tttagcatgt	60
gtctggatac	gggtggtttac	aggtactgat	ccgggaacag	gaacaagcgc	ttgtcgaagg	120
gcaagaagg	tgtaagaag	aggaccgttg	atcctttctc	caggaaggac	gaatactctg	180
ttaaggatat	tcgacgtgga	ctgtgtaagt	cgaccgcagc	taatctatat	caggcgcctt	240
ccactttcca	gatcagagag	tatgttgca	gcataatgatg	tcgaattgca	ggataaaggc	300
gattcacaat	ggtagtggag	attatgctga	ctgaattata	gtgtcgggaa	gactctggtc	360
aaccgcacca	gtggtctcaa	gaacgccaat	gactccctga	agggtcgaat	tttcgaggtc	420
tcgctggctg	acctgcagaa	tgatgaagac	catgctttcc	gcaagggttaa	gcttcgtgtg	480
gacgaggttc	agggcaagaa	ctgtttgacc	aacttccacg	gtcttgattt	cacaaccgac	540
aaattgcgat	ccctcgtgcg	caagtggcag	tcgctgatcg	aagccaatgt	caactgtgaag	600
acgaccgatg	attatctcct	tcggcttttt	gctatcgctt	tcaccaagag	acgcccgaac	660
cagattaaga	agaccacata	tgctcggttct	tctcaaatacc	gtgccatccg	caagaagatg	720
attgaaatca	tgagagggga	ggcagccagc	tgctctctcg	ctcagctcac	tcacaagctc	780
attcctgagg	tcattgggtcg	tgagatcgag	aaggctaccc	agggaatcta	tcctttgcag	840
aatgtgtgtg	accctgttat	tcttactcgg	gatgaagact	aactgcaatc	taggtccata	900
ttcgcaaggt	caagcttctt	aaggctccca	agttcgacct	gggtgcactg	ctgaatctgc	960
acggtgaatc	tacaaccgat	gataagggcc	acaaggtcga	gagagagttc	aaggagcagg	1020
ttctcgaaag	cgttttaa					1037

<210> 153

<211> 771

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA262; clone 10-2-18

Coding region without introns

<400> 153

atggcggttg	gaaagaacaa	gcgcttgctg	aagggcaaga	aggggtgttaa	gaagaggacc	60
gttgatcctt	tctccaggaa	ggacgaatac	tctgttaagg	cgccttccac	tttccagatc	120
agagatgtcg	ggaagactct	ggtcaaccgc	accagtggtc	tcaagaacgc	caatgactcc	180
ctgaagggtc	gaattttcga	ggtctcgctg	gctgacctgc	agaatgatga	agacctgct	240

```

ttccgcaagg ttaagcttcg tgtggacgag gttcagggca agaactgttt gaccaacttc 300
cacgggtcttg atttcacaac cgacaaattg cgatccctcg tgcgcaagtg gcagtcgctg 360
atcgaagcca atgtcactgt gaagacgacc gatgattatc tccttcggct ttttgctatc 420
gccttcacca agagacgccc gaaccagatt aagaagacca catatgctcg ttcttctcaa 480
atccgtgcca tccgcaagaa gatgattgaa atcatgcaga gggaggcagc cagctgctct 540
ctcgctcagc tcaactacaa gctcattcct gaggtcattg gtcgtgagat cgagaaggct 600
acccagggaa tctatccttt gcagaatgtc catattcgca aggtcaagct tcttaaggct 660
cccaagttcg acctgggtgc actgctgaat ctgcacggtg aatctacaac cgatgataag 720
ggccacaagg tcgagagaga gttcaaggag caggttctcg aaagcgttta a 771

```

<210> 154

<211> 256

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA262; clone 10-2-18
Protein sequence

<400> 154

```

Met Ala Val Gly Lys Asn Lys Arg Leu Ser Lys Gly Lys Lys Gly Val
1          5          10          15
Lys Lys Arg Thr Val Asp Pro Phe Ser Arg Lys Asp Glu Tyr Ser Val
20          25          30
Lys Ala Pro Ser Thr Phe Gln Ile Arg Asp Val Gly Lys Thr Leu Val
35          40          45
Asn Arg Thr Ser Gly Leu Lys Asn Ala Asn Asp Ser Leu Lys Gly Arg
50          55          60
Ile Phe Glu Val Ser Leu Ala Asp Leu Gln Asn Asp Glu Asp His Ala
65          70          75          80
Phe Arg Lys Val Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Cys
85          90          95
Leu Thr Asn Phe His Gly Leu Asp Phe Thr Thr Asp Lys Leu Arg Ser
100         105         110
Leu Val Arg Lys Trp Gln Ser Leu Ile Glu Ala Asn Val Thr Val Lys
115         120         125
Thr Thr Asp Asp Tyr Leu Leu Arg Leu Phe Ala Ile Ala Phe Thr Lys
130         135         140
Arg Arg Pro Asn Gln Ile Lys Lys Thr Thr Tyr Ala Arg Ser Ser Gln
145         150         155         160
Ile Arg Ala Ile Arg Lys Lys Met Ile Glu Ile Met Gln Arg Glu Ala
165         170         175
Ala Ser Cys Ser Leu Ala Gln Leu Thr His Lys Leu Ile Pro Glu Val
180         185         190
Ile Gly Arg Glu Ile Glu Lys Ala Thr Gln Gly Ile Tyr Pro Leu Gln
195         200         205

```

Asn Val His Ile Arg Lys Val Lys Leu Leu Lys Ala Pro Lys Phe Asp
 210 215 220

Leu Gly Ala Leu Leu Asn Leu His Gly Glu Ser Thr Thr Asp Asp Lys
 225 230 235 240

Gly His Lys Val Glu Arg Glu Phe Lys Glu Gln Val Leu Glu Ser Val
 245 250 255

<210> 155

<211> 1819

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 155

aattcatcag	cataacgaac	ccccaacgac	ttcgaaaaaa	aagcccgatt	cgaaagaatt	60
gcgcattcaa	cataccatgg	tgggcggctt	cgtgtcgtgt	cgtacgggta	ttgtcgacaa	120
tgaggattga	agatgggcca	ggtcaatttg	ggatgttcgt	tgtgggacta	gggttttttt	180
ctgtgttggt	gcggtcacgc	tgcggctggg	ctaagcgggc	acgtgactgt	ggctgactgc	240
ctggtgacgc	ccccccccgg	aggaaccccc	aaccggcagc	cagataggct	cgggaggatc	300
atcgtcgaat	gatggcattg	ttcttgggtc	cagtggatgg	gttattaatg	actgcctgga	360
cggctggatg	actccgtcgc	tgatttagca	ttgtgatcca	cgatttatgt	ttcatttctg	420
gggcgcgggt	ttactaccat	cacttttgtc	actaccatca	cttttatact	gagtttctga	480
ccccgacccc	gaaccagact	atggcaactt	cgactgggac	cggatgggct	cagctccggc	540
agcaagcccc	ttcgcttgag	actcagggtac	ggaactcgaa	actacgctat	aatgaggcct	600
tactcgtgat	ttggatgttg	acaataatgt	tcctagaccg	agagtctgtt	tcacacctat	660
gcgcagtatg	catcgatgac	gaagctgcct	ccgaaaccct	cagaagaaga	acaacggatt	720
gaatcgcaac	tgaaggatct	tcttgaaaag	gtgtgcaact	tgaggccctc	tagtccagcc	780
caacagacga	tcatgctgac	acgatccgat	catagcgtga	agccctcatc	tcccagctct	840
cccgtctcct	tgactccgaa	gccactctta	ccgcactctgc	cctgaaacag	agcaatcttg	900
cccgcaatcg	cgaagtccct	caggatcatc	gccgcgaatt	gcagcgcctg	aacgcgcgaa	960
tcgccgagtc	ccgcgaccca	gccaatcttc	tgtctaactg	ccgctccgac	attgatgcct	1020
accgcaattc	aaaccccgcc	gcggctgagg	cagactacat	gctcgaggag	cgggggtcgta	1080
tagatgaaag	ccataacatg	atagatggtg	tcctaagcca	ggcgtatgca	atcaacgaga	1140
gttttgggct	acaacgtgaa	accctggcca	gcataaatcg	ccgtatcgtc	ggtgctgcca	1200
ataaggtacc	aggaatgaat	gcattgattg	gtaagattgg	gacgaagagg	agacgtgacg	1260
caatcatctt	gggggctttc	atcggctttt	gtttcttgat	ggtgttcttc	ttccgatgag	1320
atgctgggtg	tccgtataacc	gccgatcttc	ctgtgttata	attccttgct	caacgttatc	1380
tacatcggag	accgcacggc	gttcgggtgt	tttcatgtac	tccttttctg	catgcaagca	1440
ctaatacaca	tggtcatggc	gtttcagggt	gtctatttca	catttatgta	catacagggt	1500
cagactgctg	tagccctagg	gtcaccgca	tgatcactct	tggtttcgga	cttgcggtt	1560
caccttggtt	tcttcccgcc	cattcctcag	ccggtagctt	cgactcgaga	ctgattcttc	1620
tctcctggat	taattttgcga	accccgttgt	tcaatccgtc	tagctcgccct	tcctctgccg	1680
gcccgtatcc	cgcccatcgg	atgacgacgt	tctcgtccag	cagatagaca	taaccaactt	1740
tactgttcat	cattccgatt	gcttctttca	acccatccgt	aagacctttg	cgcacaagga	1800
aataccgttc	gtgctgctc					1819

<210> 156

<211> 819

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250
 Genomic sequence containing the coding region

```

<400> 156
atggcaactt cgactgggac cggatgggct cagctccggc agcaagcccg ttcgcttgag    60
actcaggtac ggaactcgaa actacgctat aatgaggctt tactcgtgat ttggatgttg    120
acaataatgt tcctagaccg agagtctgtt tcacacctat gcgcagtatg catcgatgac    180
gaagctgcct ccgaaaccct cagaagaaga acaacggatt gaatcgcaac tgaaggatct    240
tcttgaaaag gtgtgcactt tgaggccctc tagtccagcc caacagacga tcatgctgac    300
acgatccgat catagcgtga agccctcatc tcccagctct cccgtctcct tgactccgaa    360
gccactctta ccgcatctgc cctgaaacag agcaatcttg cccgcaatcg cgaagtcctc    420
caggatcatc gccgcgaatt gcagcgccctg aacgccgcaa tcgccgagtc ccgcgaccga    480
gccaatcttc tgtctaacgt ccgctccgac attgatgcct accgcaattc aaaccccgcc    540
gcggctgagg cagactacat gctcgaggag cggggtcgta tagatgaaag ccataacatg    600
atagatggtg tcctaagcca ggcgatgca atcaacgaga gttttgggct acaacgtgaa    660
accctggcca gcatcaatcg ccgtatcgtc ggtgctgcca ataaggtacc aggaatgaat    720
gcattgattg gtaagattgg gacgaagagg agacgtgacg caatcatctt gggggctttc    780
atcggtttt gtttcttgat ggtgttcttc ttccgatga    819

```

<210> 157

<211> 684

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250
Coding region without introns

```

<400> 157
atggcaactt cgactgggac cggatgggct cagctccggc agcaagcccg ttcgcttgag    60
actcagaccg agagtctgtt tcacacctat gcgcagtatg catcgatgac gaagctgcct    120
ccgaaaccct cagaagaaga acaacggatt gaatcgcaac tgaaggatct tcttgaaaag    180
cgtgaagccc tcatctccca gctctcccg tctcttgact ccgaagccac tcttaccgca    240
tctgccttga aacagagcaa tcttgcccg aatcgcgaa tcttccagga tcatcgccgc    300
gaattgcagc gcctgaacgc cgcaatcgcc gagtcccgcg accgagccaa tcttctgtct    360
aacgtccgct ccgacattga tgctaccgc aattcaaacc ccgccgcgcc tgaggcagac    420
tacatgctcg aggagcgggg tcgtatagat gaaagccata acatgataga tgggtgccta    480
agccaggcgt atgcaatcaa cgagagtttt gggctacaac gtgaaaccct ggccagcatc    540
aatcgccgta tcgtcggtgc tgccaataag gtaccaggaa tgaatgcatt gattggtaag    600
attgggacga agaggagacg tgacgcaatc atcttggggg ctttcatcgg cttttgtttc    660
ttgatggtgt tcttcttccg atga    684

```

<210> 158

<211> 227

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250
Protein sequence

<400> 158

Met Ala Thr Ser Thr Gly Thr Gly Trp Ala Gln Leu Arg Gln Gln Ala
1 5 10 15

Arg Ser Leu Glu Thr Gln Thr Glu Ser Leu Phe His Thr Tyr Ala Gln
20 25 30

Tyr Ala Ser Met Thr Lys Leu Pro Pro Lys Pro Ser Glu Glu Glu Gln
35 40 45

Arg Ile Glu Ser Gln Leu Lys Asp Leu Leu Glu Lys Arg Glu Ala Leu
 50 55 60
 Ile Ser Gln Leu Ser Arg Leu Leu Asp Ser Glu Ala Thr Leu Thr Ala
 65 70 75 80
 Ser Ala Leu Lys Gln Ser Asn Leu Ala Arg Asn Arg Glu Val Leu Gln
 85 90 95
 Asp His Arg Arg Glu Leu Gln Arg Leu Asn Ala Ala Ile Ala Glu Ser
 100 105 110
 Arg Asp Arg Ala Asn Leu Leu Ser Asn Val Arg Ser Asp Ile Asp Ala
 115 120 125
 Tyr Arg Asn Ser Asn Pro Ala Ala Ala Glu Ala Asp Tyr Met Leu Glu
 130 135 140
 Glu Arg Gly Arg Ile Asp Glu Ser His Asn Met Ile Asp Gly Val Leu
 145 150 155 160
 Ser Gln Ala Tyr Ala Ile Asn Glu Ser Phe Gly Leu Gln Arg Glu Thr
 165 170 175
 Leu Ala Ser Ile Asn Arg Arg Ile Val Gly Ala Ala Asn Lys Val Pro
 180 185 190
 Gly Met Asn Ala Leu Ile Gly Lys Ile Gly Thr Lys Arg Arg Arg Asp
 195 200 205
 Ala Ile Ile Leu Gly Ala Phe Ile Gly Phe Cys Phe Leu Met Val Phe
 210 215 220
 Phe Phe Arg
 225

<210> 159

<211> 2601

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 159

tataatttct	gaactgtaga	ctccaaattg	caaatcctct	cgcctttcaa	gtgattccac	60
tctgcctcc	tttctgtctt	ctttttttcc	cctttttatc	ttttcatttt	atcatctttg	120
ttactgtttt	cccaaacgaa	tccattatta	tttctttccc	ttggagggtc	cctactgtgg	180
tcttgtgtct	gcactcttgc	caagcccatt	ggtccttgct	ctgagcctat	cacttgcgat	240
tcgcccgc	ataagtcgc	ctctctcaac	ctttccatct	cacgcgcacc	tccactcaac	300
atccaccatt	cggatattcc	gcccatccaa	agcgaacacc	cctccttctg	ctccaccatc	360
gattgcagtc	tgcccaaaac	ggacttcaga	actcccttct	acgctatttt	ccgccattca	420
ctgttgaagt	gcagccctcc	atactctcga	tagcaactgc	ccaaccccc	tcttactgcc	480
aacccccacaa	gttgcccggtg	atgtcacaaa	atcgacctgg	ggtgttctcg	aatctgcgca	540
tgggtggtaa	ggaacatcca	aatgctgagt	ccaattgttc	agaaaacatt	accaggagc	600
ctgtggaact	aactgctttg	ctttccgacc	atacagaagt	cgtccgcgag	aagggtccagg	660
atggactgac	aggggaaact	aaggagattt	cgtactcaca	atgtaaaatc	gtcggcaatg	720
gatcgtttgg	tgtcgtcttt	cagacgaaaa	tgatgccaag	cggcgaggat	gctgccatta	780
agagggtcct	tcaagacaag	cgcttcaaag	tatgtgtaca	ttataagggc	aattgccttc	840

gctgcccac	ccaaagatac	tgtcgctgac	gagataccag	aatcgagaac	tgacagattat	900
gcggtattgt	cgccatccta	acatcgtaga	attgaaagcc	ttctattact	cgaacggcga	960
gagggtatgc	gactctcctt	tgtctcccca	ttcggttctag	tttgccgttt	gctgactacc	1020
ctaccattgt	ctttcacaga	aggatgaagt	gtacctaaac	ctcggttctcg	aatacgtacc	1080
agaaaccgtg	tatcgggcgt	cgcggtactt	taataaactc	aaaacgacta	tgccaatggt	1140
ggaagtcaag	ctgtatatct	atcaattggt	ccgttccctg	gcatacatcc	attcacaagg	1200
catctgccac	cgtgacatca	agccccagaa	tctcttactt	gatccatcca	ccggcatcct	1260
caaactctgc	gacttttggt	cgccaagat	tctggtagag	aatgagccca	acgtttccta	1320
tatctgttcc	cgctactatc	gtgcgcggga	attgatcttt	ggcgccacta	attacacaac	1380
aaagatcggg	aagtcttgac	tgattcctcc	ttcaagtttg	gtactgtcat	gctgacgac	1440
gtcaagacgt	gtggtccacg	gggtgtgtga	tggctgaact	catgcttggg	cagccattgt	1500
tccctggaga	gtcgggaatt	gaccaactgg	tggaaatcat	caaggttctt	ggaaccctta	1560
ctcgggagca	gatccgcacc	atgaacccaa	actatatgga	gcacaaattc	cctcaaataca	1620
agccacaccc	attcaacaag	gtgaccacgc	tcttaaagaa	cttcttgcca	atatgcactg	1680
acttgatgac	cccagggtttt	ccggagagct	cctcacgagg	ccattgatct	gatctcagct	1740
ttgctagaat	acacgccgac	acaacgtctc	tccgctatcg	aggcgatgtg	ccaccggttc	1800
ttcgacgaac	tcagagatcc	caatacgcga	ctgcccgaact	ctcggcaccc	tggtggcgct	1860
gctagagacc	tcccaatctc	ctttgatttc	tccagacatg	gtttgttgtc	acttgaggcc	1920
caaattcatt	cttccagatg	gcttattcgc	tgatcactct	ttttagaac	tttctattgc	1980
acctgcattg	aacagccggc	tggttccccc	tcatgcacgc	gccgctctcg	aggcccgggg	2040
gctagacatt	gacaacttca	ctcctctcac	gaaggaggag	atgatggcac	gtctcgactg	2100
agtcgatacg	tttctcggtt	cgaatcaaac	gccccctcga	tagtgcttat	atccgcacaa	2160
ctgcgcgagg	atatgatgtc	atgcgatgca	ttttgctttg	tgaactggga	tgctccttga	2220
ccagaagtgg	cttttatgga	acttgctgac	cagagtcgct	gactagacac	ccgggagttg	2280
gcacttttcc	cgaacgtatg	aggatacaag	gcaaattcccc	atatttaaaa	gaaaaaggag	2340
aaaaacaggag	aaaaaaaaag	aatgggaaat	acagaaacat	cgcatctctg	tcacaacata	2400
agcgggtttc	gtgaggcggg	gggtgcatcat	tgcaaatatca	tgcaacgggg	ttgagggaatt	2460
gtcatagtct	ggagttttcg	aggtgtctga	gacagctctt	gggaaaggaa	aaaaagtgat	2520
accctttagt	gtgcgagtct	gccttcgggg	atttaagttt	gcatagcttc	attctcgttt	2580
gaaggaggac	atgaccattc	c				2601

<210> 160

<211> 1601

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439

Genomic sequence containing the coding region

<400> 160

atgtcacaaa	atcgacctgg	gggtgttctcg	aatctgcgca	tgggtggtaa	ggaacatcca	60
aatgctgagt	ccaattgttc	agaaaacatt	acccaggagc	ctgtggaact	aactgctttg	120
ctttccgacc	atacagaagt	cgctccgcgag	aagggtccagg	atggactgac	aggggaaact	180
aaggagattt	cgtactcaca	atgtaaaatc	gtcggcaatg	gatcgtttgg	tgctcgtctt	240
cagacgaaaa	tgatgccaag	cggcgaggat	gctgccatta	agagggtcct	tcaagacaag	300
cgcttcaaa	tatgtgtaca	ttataagggc	aattgccctc	gctgcccac	ccaaagatac	360
tgtcgctgac	gagataccag	aatcgagaac	tgacagattat	gcggtattgt	cgccatccta	420
acatcgtaga	attgaaagcc	ttctattact	cgaacggcga	gagggtatgc	gactctcctt	480
tgtctcccca	ttcggttctag	tttgccgttt	gctgactacc	ctaccattgt	ctttcacaga	540
aggatgaagt	gtacctaaac	ctcggttctcg	aatacgtacc	agaaaccgtg	tatcgggcgt	600
cgcggtactt	taataaactc	aaaacgacta	tgccaatggt	ggaagtcaag	ctgtatatct	660
atcaattggt	ccgttccctg	gcatacatcc	attcacaagg	catctgccac	cgtgacatca	720
agccccagaa	tctcttactt	gatccatcca	ccggcatcct	caaactctgc	gacttttggt	780
cgccaagat	tctggtagag	aatgagccca	acgtttccta	tatctgttcc	cgctactatc	840
gtgcgcggga	attgatcttt	ggcgccacta	attacacaac	aaagatcggg	aagtcttgac	900
tgattcctcc	ttcaagtttg	gtactgtcat	gctgacgac	gtcaagacgt	gtggtccacg	960
gggtgtgtga	tggctgaact	catgcttggg	cagccattgt	tccctggaga	gtcgggaatt	1020
gaccaactgg	tggaaatcat	caaggttctt	ggaaccctta	ctcgggagca	gatccgcacc	1080
atgaacccaa	actatatgga	gcacaaattc	cctcaaataca	agccacaccc	attcaacaag	1140

```

gtgaccacgc tcttaaagaa cttcttgcca atatgcactg acttgatgac cccagggttt 1200
ccggagagct cctcacgagg ccattgatct gatctcagct ttgctagaat acacgccgac 1260
acaacgtctc tccgctatcg aggcgatgtg ccacccgttc ttcgacgaac tcagagatcc 1320
caatacgcga ctgcccgaact ctccggcacc tgggtggcgt gctagagacc tccccaatct 1380
ctttgatttc tccagacatg gtttgttgct acttgaggcc caaattcatt cttccagatg 1440
gcttattcgc tgatcactct tttgtagaac tttctattgc acctgcattg aacagccggc 1500
tggttcccc tcatgcacgc gccgctctcg aggcccggg gctagacatt gacaacttca 1560
ctcctctcac gaaggaggag atgatggcac gtctcgactg a 1601

```

<210> 161

<211> 1185

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439
Coding region without introns

<400> 161

```

atgtcacaaa atcgacctgg ggtgttctcg aatctgcgca tgggtgaagt cgtccgcgag 60
aagggtccagg atggactgac aggggaaact aaggagattt cgtactcaca atgtaaaatc 120
gtcggcaatg gatcgtttgg tgcgtcttt cagacgaaaa tgatgccaa ggcgcaggat 180
gctgccatta agagggctct tcaagacaag cgcttcaaaa atcgagaact gcagattatg 240
cggattgttc gccatcctaa catcgtagaa ttgaaagcct tctattactc gaacggcgag 300
aggaaggatg aagtgtacct aaacctcgtt ctccaatacg taccagaaac cgtgtatcgg 360
gcgtcgcggt actttaataa actcaaaacg actatgccaa tgttggaagt caagctgtat 420
atctatcaat tgttccgttc cctggcatac atccattcac aaggcatctg ccaccgtgac 480
atcaagcccc agaattctct acttgatcca tccaccggca tctcaaaact ctgcgacttt 540
ggttcggcca agattctggt agagaatgag cccaacgttt cctatatctg tccccgctac 600
tatcgtgcgc cggaattgat ctttggcgcc actaattaca caacaaagat cgacgtgtgg 660
tccacgggtt gtgtgatggc tgaactcatg cttggtcagc cattgttccc tggagagtcg 720
ggaattgacc aactgggtgga aatcatcaag gttcttgga cccctactcg ggagcagatc 780
cgcaccatga acccaaaacta tatggagcac aaattccctc aaatcaagcc acaccattc 840
aacaagggtt tccggagagc tcctcacgag gccattgatc tgatctcagc tttgctagaa 900
tacacgccga cacaacgtct ctccgctatc gaggcgatgt gccaccggtt cttcgacgaa 960
ctcagagatc ccaatacgcg actgccgcac tctcggcacc ctggtggcgc tgctagagac 1020
ctccccaatc tctttgattt ctccagacat gaactttcta ttgcacctgc attgaacagc 1080
cggctgggtc cccctcatgc acgcgccgct ctcgaggccc gggggctaga cattgacaac 1140
ttcactctc tcacgaagga ggagatgatg gcacgtctcg actga 1185

```

<210> 162

<211> 394

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439
Protein sequence

<400> 162

```

Met Ser Gln Asn Arg Pro Gly Val Phe Ser Asn Leu Arg Met Gly Glu
1          5          10          15

Val Val Arg Glu Lys Val Gln Asp Gly Leu Thr Gly Glu Thr Lys Glu
20          25          30

Ile Ser Tyr Ser Gln Cys Lys Ile Val Gly Asn Gly Ser Phe Gly Val
35          40          45

```


Val Phe Gln Thr Lys Met Met Pro Ser Gly Glu Asp Ala Ala Ile Lys
 50 55 60
 Arg Val Leu Gln Asp Lys Arg Phe Lys Asn Arg Glu Leu Gln Ile Met
 65 70 75 80
 Arg Ile Val Arg His Pro Asn Ile Val Glu Leu Lys Ala Phe Tyr Tyr
 85 90 95
 Ser Asn Gly Glu Arg Lys Asp Glu Val Tyr Leu Asn Leu Val Leu Glu
 100 105 110
 Tyr Val Pro Glu Thr Val Tyr Arg Ala Ser Arg Tyr Phe Asn Lys Leu
 115 120 125
 Lys Thr Thr Met Pro Met Leu Glu Val Lys Leu Tyr Ile Tyr Gln Leu
 130 135 140
 Phe Arg Ser Leu Ala Tyr Ile His Ser Gln Gly Ile Cys His Arg Asp
 145 150 155 160
 Ile Lys Pro Gln Asn Leu Leu Leu Asp Pro Ser Thr Gly Ile Leu Lys
 165 170 175
 Leu Cys Asp Phe Gly Ser Ala Lys Ile Leu Val Glu Asn Glu Pro Asn
 180 185 190
 Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala Pro Glu Leu Ile Phe
 195 200 205
 Gly Ala Thr Asn Tyr Thr Thr Lys Ile Asp Val Trp Ser Thr Gly Cys
 210 215 220
 Val Met Ala Glu Leu Met Leu Gly Gln Pro Leu Phe Pro Gly Glu Ser
 225 230 235 240
 Gly Ile Asp Gln Leu Val Glu Ile Ile Lys Val Leu Gly Thr Pro Thr
 245 250 255
 Arg Glu Gln Ile Arg Thr Met Asn Pro Asn Tyr Met Glu His Lys Phe
 260 265 270
 Pro Gln Ile Lys Pro His Pro Phe Asn Lys Val Phe Arg Arg Ala Pro
 275 280 285
 His Glu Ala Ile Asp Leu Ile Ser Ala Leu Leu Glu Tyr Thr Pro Thr
 290 295 300
 Gln Arg Leu Ser Ala Ile Glu Ala Met Cys His Pro Phe Phe Asp Glu
 305 310 315 320
 Leu Arg Asp Pro Asn Thr Arg Leu Pro Asp Ser Arg His Pro Gly Gly
 325 330 335
 Ala Ala Arg Asp Leu Pro Asn Leu Phe Asp Phe Ser Arg His Glu Leu
 340 345 350
 Ser Ile Ala Pro Ala Leu Asn Ser Arg Leu Val Pro Pro His Ala Arg
 355 360 365

Ala Ala Leu Glu Ala Arg Gly Leu Asp Ile Asp Asn Phe Thr Pro Leu
 370 375 380

Thr Lys Glu Glu Met Met Ala Arg Leu Asp
 385 390

<210> 163

<211> 2539

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 163

ttgaggattt	gcggaacctt	cacgatggca	cttgacacca	caatagcaat	acccagagcc	60
ttggagatag	caagagacgt	gcaggcagca	tccttgggtga	catccagatc	gaggaggagg	120
gcgctgtggc	atggcgatcc	gatcagggag	atgatgacat	cgtggacagg	ttgtgggaga	180
gcggacgaga	taggacggag	aacgggttga	agagggtcaa	taacgaccct	ttgaagcgta	240
tccatggcga	gagttctacag	ggcaaaagac	ggctcagggc	cttggttgaa	gaggagtttg	300
ccaacgggagc	acggtgggttc	caaaagatca	gcaacaacca	tcgggacgga	atggtgcatt	360
cattcctgcg	gttgtgggtct	ctgtgcctcg	ccggggaatt	tctgccctgt	caatcgcgac	420
tcttccgaga	ctcactatct	catgatctag	atctcgtcct	atcgtgattt	caatatccct	480
ccgtccatgt	tccttccgcc	atgatttatt	tccggtcctc	gttgctgagg	tctggattgg	540
ctcgagatcc	tgctcgcctg	tgttcacaat	gcttctcacg	actctcacca	tcacgacgac	600
ctgtcgcagt	tcgcagcttc	ttctcctcat	ctcggctgcg	ggctggcatt	gccgatcatg	660
aatcaactcc	ctcgactgtc	caaaagacct	atttttctgc	caatcggacc	gcagatggct	720
tacttgcatc	cttatccgcc	gtcaatagct	cccctcgaag	tattgccgac	aatgcgttat	780
cacagggtgc	agccagttcg	gagtcgatta	cttcacagtc	tacttcacaa	gagttacctc	840
atcgccggag	gaagcggtta	aaggaagagg	cggccaagaa	taatgctgca	gaaaccgaac	900
tccctcctga	tgccctcgtct	caattgtcca	ccctctcatc	agccctccct	gcgacttccc	960
tgccgccgcaa	gctggctgcg	tttctcgccc	tcacaaagcc	tcgtctctcg	ttcctgatcg	1020
tggtgacgac	tacctccgct	tatgggatgt	acccgatctc	ctctcttctc	acacttgacc	1080
cttcaatgac	tcccctaccg	accctctcga	cctcaacctt	gacctttctc	tacctgacca	1140
caggaaacctt	cttgtcttca	tgacgcgcca	ataccttgaa	tatgctcctt	gaacctaaat	1200
acgatgccct	catgtcacgg	acacggaacc	ggcggtagt	gcgggggcta	ctctcacgcc	1260
gtgctgcggt	attgtttgcg	attgcgactg	ctgctgcagg	tctcggtttg	ttatacattg	1320
gaacgaaccc	tacgactact	gcgctctccg	ccagtaatat	ctgtctctat	gcctttgtgt	1380
atacgccgct	gaagcgtata	tcagtgatca	acacctgggt	aggcgccgtg	gtaggaggca	1440
ttcctccggt	gatgggttgg	accgctgcag	caggccagac	agcgaccact	ggccacgaca	1500
gctggcgggga	catgttggtc	agcaaggata	gcctcgggtg	ttggctcctg	ggtggcattc	1560
tctttgcatg	gcagtttccct	catttcaatg	ctttgtccta	catgatccgt	gaagagtaca	1620
aggcagccgg	gtacaggatg	ctcgcatgga	ctaataccgc	cgcaaatgcc	cgtgtcgcac	1680
tacgatattc	tcttctcatg	tttctttctt	ccgtcgggtc	ctgggtgggtg	ggagttgtcg	1740
gtaatggttt	cctggttggga	agcacggcgg	ccaatggctg	gctagtcaaa	gaggcctaca	1800
aattctggcg	gcaccaaggc	gccaacggca	gtgctcgacg	cctcttcttg	gccagtattt	1860
ggcagctgcc	aatcctcctt	gtcggtggtc	tggtcacgaa	gaaaggctct	tgggatgggtg	1920
tctggaacaa	tgttttcggg	cagcctgtgg	aagacgagga	tgactatctc	tgggaggatg	1980
aggatgaagt	ggcagaggcg	gagcgcaaga	tgataacctg	gaagacgagt	agctcgtgat	2040
tcttactttt	gtttatcagc	gcaattcgac	actgatattg	ttttgtttac	agcactttat	2100
catactagac	tgccctttttg	gcatgggagg	ctggcgctcg	tgtataacaa	attcttttta	2160
aacttcactc	atgatgatcc	gcaacacgta	gatatagctt	caacatgaat	tgattcaggt	2220
agttttctgt	atagcacctt	aaacgggggg	ttcttgctat	atcgaacctc	taccccaact	2280
tataagattg	agttctgtat	cacaatctac	ttgcacttaa	accaagacta	tatcgggtgtt	2340
tctatgagac	aactattttac	agatcgcccc	cgtgagaaga	gattgggtat	catgtctatc	2400
ctaattgtaca	attcagctga	gcggettgcg	gcaactgcat	cttcatacac	tcattcatcc	2460
tttaaacgaa	gatggtaggt	ttctaattgt	tctttcgtca	tcatgctagg	agccttgacc	2520
atggcatcat	cgccacctt					2539

<210> 164
 <211> 1539
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190
 Genomic sequence containing the coding region

<400> 164
 atgatttata tccggtcctc gttgctgagg tctggattgg ctcgagatcc tgctcgcttg 60
 tgttcacaat gcttctcacg actctcacca tcacgacgac ctgtcgagct tcgcagcttc 120
 ttctcctcat ctcggtcgcg ggttggcatt gccgatcatg aatcaactcc ctcgactgtc 180
 caaaagacct atttttctgc caatcggaac gcagatggct tacttgcatc cttatccgcc 240
 gtcaatagct cccctcgaag tattgccgac aatgcgttat cacagggtgc agccagttcg 300
 gagtcgatta cttcacagtc tacttcacaa gagttacctc atcgccggag gaagcgggta 360
 aaggaagagg cggccaagaa taatgctgca gaaaccgaac tccctcctga tgccctcgct 420
 caattgtcca cctctctcgc agccctccct gcgacttccc tgcgccgcaa gctggctgcg 480
 tttctcgccc tcacaaagcc tcgtctctcg ttcttgatcg tgttgacgac tacctccgct 540
 tatgggatgt acccgatctc ctctcttctc acacttgacc cttcaatgac tcccctaccg 600
 accctctcga cctcaacctt gacctttctc tacctgacca caggaacctt cttgtcttca 660
 tgcagcgcca ataccttgaa tatgctcctt gaacctaaat acgatgccct catgtcacgg 720
 acacggaacc ggccgttagt gcgggggcta ctctcacgcc gtgctgcggt attgtttgcg 780
 attgcgactg ctgctgcagg tctcggtttg ttatacattg gaacgaacct tacgactact 840
 ggcgtctccg ccagtaatat ctgtctctat gcctttgtgt atacgccgct gaagcgtata 900
 tcagtgatca acacctgggt aggcgccgtg gtaggaggca ttcctccggt gatgggttg 960
 accgctgcag caggccagac agcgaccact ggccacgaca gctggcgga catgttggtc 1020
 agcaaggata gcacgggtgg ttggctcctg ggtggcattc tctttgcatg gcagtttctc 1080
 catttcaatg ctttgtccta catgatccgt gaagagtaca aggcagccgg gtacaggatg 1140
 ctgcgatgga ctaatccgc cgcaaatgcc cgtgtcgac tacgatattc tcttctcatg 1200
 tttcctttct ccgtcggtct ctgggtggta ggagttgtcg gtaatgggtt cctgggttgga 1260
 agcacggcgg ccaatggctg gctagtcaaa gaggcctaca aattctggcg gcaccaaggc 1320
 gccaacggca gtgctcgacg cctcttcttg gccagtattt ggcagctgcc aatcctcctt 1380
 gtcgggtggtc tggtcacgaa gaaaggtctc tgggatgggt tctggaacaa tgttttcggt 1440
 cagcctgtgg aagacgagga tgactatctc tgggaggatg aggatgaagt ggcagaggcg 1500
 gagcgcaaga tgatacctgc gaagacgagt agctcgtga 1539

<210> 165
 <211> 1539
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190
 Coding region without introns

<400> 165
 atgatttata tccggtcctc gttgctgagg tctggattgg ctcgagatcc tgctcgcttg 60
 tgttcacaat gcttctcacg actctcacca tcacgacgac ctgtcgagct tcgcagcttc 120
 ttctcctcat ctcggtcgcg ggttggcatt gccgatcatg aatcaactcc ctcgactgtc 180
 caaaagacct atttttctgc caatcggaac gcagatggct tacttgcatc cttatccgcc 240
 gtcaatagct cccctcgaag tattgccgac aatgcgttat cacagggtgc agccagttcg 300
 gagtcgatta cttcacagtc tacttcacaa gagttacctc atcgccggag gaagcgggta 360
 aaggaagagg cggccaagaa taatgctgca gaaaccgaac tccctcctga tgccctcgct 420
 caattgtcca cctctctcgc agccctccct gcgacttccc tgcgccgcaa gctggctgcg 480
 tttctcgccc tcacaaagcc tcgtctctcg ttcttgatcg tgttgacgac tacctccgct 540
 tatgggatgt acccgatctc ctctcttctc acacttgacc cttcaatgac tcccctaccg 600
 accctctcga cctcaacctt gacctttctc tacctgacca caggaacctt cttgtcttca 660
 tgcagcgcca ataccttgaa tatgctcctt gaacctaaat acgatgccct catgtcacgg 720

```

acacggaacc ggccgttagt gcgggggcta ctctcacgcc gtgctgcggt attgtttgcg      780
attgcgactg ctgctgcagg tctcggtttg ttatacattg gaacgaaccc tacgactact      840
gcgctctccg ccagtaatat ctgtctctat gcctttgtgt atacgccgct gaagcgtata      900
tcagtgatca acacctgggt aggcgccgtg gtaggaggca ttcctccgtt gatgggttgg      960
accgctgcag caggccagac agcgaccact ggccacgaca gctggcgagg catgttggtc     1020
agcaaggata gcatcggtgg ttggctcctg ggtggcattc tctttgcatg gcagtttcct     1080
catttcaatg ctttgtccta catgatccgt gaagagtaca aggcagccgg gtacaggatg     1140
ctcgcgatgga ctaatcccgc cgcaaatgcc cgtgtcgcac tacgatattc tcttctcatg     1200
tttcctttct ccgtcgggtct ctggtgggta ggagttgtcg gtaatggttt cctggttggg     1260
agcacggcgg ccaatggctg gctagtcaaa gaggcctaca aattctggcg gcaccaaggc     1320
gccaacggca gtgctcgacg cctcttcttg gccagtattt ggcagctgcc aatcctcctt     1380
gtcgggtggtc tggtcacgaa gaaaggtctc tgggatggtg tctggaacaa tgttttcggt     1440
cagcctgtgg aagacgagga tgactatctc tgggaggatg aggatgaagt ggcagaggcg     1500
gagcgcaaga tgatacctgc gaagacgagt agctcgtga      1539

```

<210> 166

<211> 512

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190
Protein sequence

<400> 166

```

Met Ile Tyr Leu Arg Ser Ser Leu Leu Arg Ser Gly Leu Ala Arg Asp
1              5              10              15

Pro Ala Arg Leu Cys Ser Gln Cys Phe Ser Arg Leu Ser Pro Ser Arg
20              25              30

Arg Pro Val Ala Val Arg Ser Phe Phe Ser Ser Ser Arg Leu Arg Ala
35              40              45

Gly Ile Ala Asp His Glu Ser Thr Pro Ser Thr Val Gln Lys Thr Tyr
50              55              60

Phe Ser Ala Asn Arg Thr Ala Asp Gly Leu Leu Ala Ser Leu Ser Ala
65              70              75              80

Val Asn Ser Ser Pro Arg Ser Ile Ala Asp Asn Ala Leu Ser Gln Gly
85              90              95

Ala Ala Ser Ser Glu Ser Ile Thr Ser Gln Ser Thr Ser Gln Glu Leu
100             105             110

Pro His Arg Arg Arg Lys Arg Leu Lys Glu Glu Ala Ala Lys Asn Asn
115             120             125

Ala Ala Glu Thr Glu Leu Pro Pro Asp Ala Ser Ser Gln Leu Ser Thr
130             135             140

Leu Ser Ser Ala Leu Pro Ala Thr Ser Leu Arg Arg Lys Leu Ala Ala
145             150             155             160

Phe Leu Ala Leu Thr Lys Pro Arg Leu Ser Phe Leu Ile Val Leu Thr
165             170             175

Thr Thr Ser Ala Tyr Gly Met Tyr Pro Ile Ser Ser Leu Leu Thr Leu

```

180					185					190					
Asp	Pro	Ser	Met	Thr	Pro	Leu	Pro	Thr	Leu	Ser	Thr	Ser	Thr	Leu	Thr
195					200					205					
Phe	Leu	Tyr	Leu	Thr	Thr	Gly	Thr	Phe	Leu	Ser	Ser	Cys	Ser	Ala	Asn
210					215					220					
Thr	Leu	Asn	Met	Leu	Leu	Glu	Pro	Lys	Tyr	Asp	Ala	Leu	Met	Ser	Arg
225					230					235					
Thr	Arg	Asn	Arg	Pro	Leu	Val	Arg	Gly	Leu	Leu	Ser	Arg	Arg	Ala	Ala
245					250					255					
Val	Leu	Phe	Ala	Ile	Ala	Thr	Ala	Ala	Gly	Leu	Gly	Leu	Leu	Tyr	
260					265					270					
Ile	Gly	Thr	Asn	Pro	Thr	Thr	Thr	Ala	Leu	Ser	Ala	Ser	Asn	Ile	Cys
275					280					285					
Leu	Tyr	Ala	Phe	Val	Tyr	Thr	Pro	Leu	Lys	Arg	Ile	Ser	Val	Ile	Asn
290					295					300					
Thr	Trp	Val	Gly	Ala	Val	Val	Gly	Gly	Ile	Pro	Pro	Leu	Met	Gly	Trp
305					310					315					
Thr	Ala	Ala	Ala	Gly	Gln	Thr	Ala	Thr	Thr	Gly	His	Asp	Ser	Trp	Arg
325					330					335					
Asp	Met	Leu	Phe	Ser	Lys	Asp	Ser	Ile	Gly	Gly	Trp	Leu	Leu	Gly	Gly
340					345					350					
Ile	Leu	Phe	Ala	Trp	Gln	Phe	Pro	His	Phe	Asn	Ala	Leu	Ser	Tyr	Met
355					360					365					
Ile	Arg	Glu	Glu	Tyr	Lys	Ala	Ala	Gly	Tyr	Arg	Met	Leu	Ala	Trp	Thr
370					375					380					
Asn	Pro	Ala	Ala	Asn	Ala	Arg	Val	Ala	Leu	Arg	Tyr	Ser	Leu	Leu	Met
385					390					395					
Phe	Pro	Phe	Ser	Val	Gly	Leu	Trp	Trp	Val	Gly	Val	Val	Gly	Asn	Gly
405					410					415					
Phe	Leu	Val	Gly	Ser	Thr	Ala	Ala	Asn	Gly	Trp	Leu	Val	Lys	Glu	Ala
420					425					430					
Tyr	Lys	Phe	Trp	Arg	His	Gln	Gly	Ala	Asn	Gly	Ser	Ala	Arg	Arg	Leu
435					440					445					
Phe	Trp	Ala	Ser	Ile	Trp	Gln	Leu	Pro	Ile	Leu	Leu	Val	Gly	Gly	Leu
450					455					460					
Val	Thr	Lys	Lys	Gly	Leu	Trp	Asp	Gly	Val	Trp	Asn	Asn	Val	Phe	Gly
465					470					475					
Gln	Pro	Val	Glu	Asp	Glu	Asp	Asp	Tyr	Leu	Trp	Glu	Asp	Glu	Asp	Glu
485					490					495					
Val	Ala	Glu	Ala	Glu	Arg	Lys	Met	Ile	Pro	Ala	Lys	Thr	Ser	Ser	Ser
500					505					510					

<210> 167
 <211> 2679
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
 Genomic sequence containing 3' and 5'-ends and the coding region

```

<400> 167
tcacattcac tgcaggctcg tgtactccgg agttatgcaa tgatcgctccc gtttaattat      60
cttccgaact ttggactcgt atatttttagc tgcgtgtcac ggtgatcatg atcttcattc      120
atctctttat ctgattcgat caataccggg agtactgcaa ggaggacaag tagacaggca      180
tctcgagaat tcgggtgagaa agcaaggtagc agaagagAAC tactccgtac tctgtactct      240
gtagagaaag gcaggagggtt caaacatgat tggcccggtg agaataagaa aatatcatgc      300
cttaggtcca aaggctagtgc ctacatgac cttatcagtt gactcagggt atcttatcgt      360
tgtcccagag agatgtgaag aattattgca ccggggagca cgcaaggaaa ccattctatc      420
ctatctcgtc ccttttagatt accacaggac atctacatct tgaaccttac cattccaaat      480
tacagactgc ctctgagtag atgctcaacg ccgcggttgc tgccccgcga tgttttgtat      540
atcccactga tcgcgcagca atgcgcttgg gctttgctct tcgtctctcc tctcctgcac      600
ctctcttctc aacagcacct ttccgtcgac agttgcatgc ttccggcgctc cgatcaattg      660
aacctgttat ctttcgaaat agccttgaaa agactcttga ggctcatcga tcttccaatc      720
gagccagtct gatccgcaag gtgattaacc acgattgtcc tgctgaaacg cccctccaa      780
ttttaccact tgagaatcgt gctggctcat atcaatcatc tcaaaaggcc tcttccgtgt      840
caaatgcaga gtcagagtcc ccccggtctt ctgcgcctgc gagacgagcg cagaggaagg      900
cccggttcgcc cagccaagta gccaccccg cgcacaaaag tccttggtctg aagtacttga      960
aatggcatgc agatgaaacc aagggccgac cggcacaaag tccttggtctg aagtacttga      1020
ctaccgattg gaaaacgccc gatgccgttt cgcgtctcga cgcggagatc cgcgctcttg      1080
agctctacat gacaccgacc ccgtcggagc ggactgagat agatcggctg gttgcagata      1140
tgggtagggt gctagcggga atcgtcccca gccgcgcccga ggtaaccggt tcatggcgga      1200
cgcgatttgc cttgagccac tcgggtctcg attttgtctt acctgtcccg gattcagacc      1260
gatccaccgg tgacgttcgc aagccgagtg ccacacggcc caaggtgctc cagacttaca      1320
aaaagctctt acatgaagtg ggacatgcgc ttccagagtc cccctcgctc gcggagcgag      1380
tccgcacatc aggcagccgt ttcccgcgtc tctcagccat ccacgcgccc acgggcccgc      1440
tgctgcagtt ccactgcggt gaagggtctac cggcctctgt cgaataacatc atggattacc      1500
aggccgagta tccctcgatc cggccgctct acgtgaccgc tcgctgatc ctggaggcgc      1560
ggggtaggta tggccgtact cagatgtcta ttgaatccga tgccctcgta atgcttctcg      1620
tggccttctt caaaatgaac cacgggctgt ttccagcgcc cgaactgtctc ggcgagcagc      1680
tgatcgcggt tctgcgcgcc tacggcagcg atattgacct gaccaccacc ggtgtgtccg      1740
tcgatccccc cagttggttc aatgctagta cgggtcaaacg cgccagcgcc ctgtacgcgc      1800
ccgatgatct acccgcgcat ctgcgcggcc agcgctccct catcagcctc aagagaacag      1860
cagccgccag acgcaatctg cctgccgcca gccggctgtg cgtgcaggac cccaccaatt      1920
acatgaatga tctgggcccgc agctgcgtgc gtacgttgga actccagcac acgttctcgc      1980
ttgctcatga ccgtctcggc gcaagtctca agcgtggtgga tgacagtga cgggccgcga      2040
acgttagtat cctgacagcg gccctgcaag caaacttttc tgattttgaa aatctacgcg      2100
ccaaatcgct taagctcaac gcgacctagc aatgaactgg gccagagcct tggagcttgg      2160
gacattgcag cctatcttat ttctcacttc cattactgat agtaaattat atatgagata      2220
atgtggagtc cggcaacgtg ttctcgtcac tgggctaata cctgtcactg gccactatgt      2280
agatgcagtt gactcaatag agggctcgcta taatcaaaca tcagacaatg cacgagtaga      2340
acagatggaa tatgcttgta agagaacgcc cgcttccctag tcaagcagct ctgaagagca      2400
aaacaatata tccaaacccg ctctattcga acgaaaatgc ggaaataaacc atgacagaca      2460
aagaagagac aagccaggcc agggcaaaag tatctatga catgaattca acgatcaaga      2520
tcacgcgggt gtatgagaac tccagggtta gcaataccaa caatcgacat gtatggcacc      2580
gcaaggaaaa gcaccgcgga accatacgag gatatacgat cgatcaattg ctgcccctct      2640
gtcagcagct atttccattg ctgacgggat gctgatggg      2679

```

<210> 168
 <211> 1629

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
Genomic sequence containing the coding region

<400> 168

atgctcaacg	ccgcggttgc	tgccccgcga	tgttttgtat	atcccactga	tcgcgcagca	60
atgcgcttgg	gctttgctct	tcgtctctcc	tctcctgcac	ctctcttctc	aacagcacct	120
ttccgctcgac	agttgcatgc	ttccggcgtc	cgatcaattg	aacctgttat	ctttcgaaat	180
agccttgaaa	agactcttga	ggctcatcga	tcctccaatc	gagccagtct	gatccgcaag	240
gtgattaacc	acgattgtcc	tgctgaaacg	ccccctccaa	ttttaccact	tgagaatcgt	300
gctggctcatg	atcaatcatc	tcaaaaggcc	tcctccgtgt	caaatgcaga	gtcagagtcc	360
ccccggtctt	ctgcgcctgc	gagacgagcg	cagaggaagg	cccgttcgcc	cagccaagta	420
gccaccccg	agccccagac	aacagaatat	ccacaactgc	aatggcatgc	agatgaaacc	480
aagggccgac	cggcacaaa	tccttggtg	aagtacttga	ctaccgattg	gaaaacgccc	540
gatgccgttt	cgcgtctcga	cgcggagatc	cgcgctcttg	agctctacat	gacaccgacc	600
ccgtcggagc	ggactgagat	agatcggctg	gttgcaagata	tgggtagggt	gctagcggga	660
atcgtcccca	gcccccccca	ggtaaccggt	tcattggcga	cgcgatttgc	cttgagccac	720
tcgggtctcg	attttgtctt	acctgtccc	gattcagacc	gatccaccgc	tgacgttcgc	780
aagccgagtg	ccacacggcc	caaggtgtc	cagacttaca	aaaagctctt	acatgaagt	840
ggacatgcgc	ttcagcagtc	cccctcgctc	gcggagcgag	tcgcgatcat	aggcagccgt	900
ttccccgctc	tctcagccat	ccatcgcccc	acgggcccgc	tgctgcagtt	ccactgcggt	960
gaagggctac	cggcctctgt	cgaatacatc	atggattacc	aggccgagta	tccctcgatc	1020
cggccgctct	acgtgaccgc	tcgcctgac	ctggaggcgc	ggggtaggta	tggccgtact	1080
cagatgtcta	ttgaatccga	tgccctcgta	atgcttctcg	tggccttcct	caaaatgaac	1140
cacgggcgtt	ttcagcggcc	cgactgtctc	ggcagcagc	tgatcgcgtt	tctgcgcgcc	1200
tacggcagcg	atattgacct	gaccaccacc	gggtgtgtcc	tcgatcccc	cagttgggtc	1260
aatgctagta	cggtaaaacg	cgcacgcgc	ctgtacgcgc	ccgatgatct	acccgcgc	1320
ctgcgcggcc	agcgtccct	catcagcctc	aagagaacag	cagccgccag	acgcaatctg	1380
cctgcgcgca	gccggctgtg	cgtgcaggac	cccaccaatt	acatgaatga	tctgggcccgc	1440
agctgcgtgc	gtacgttgga	actccagcac	acgttctcgc	ttgctcatga	ccgtctcggc	1500
gcaagtctca	agcgtggga	tgacagtga	ccggccgcga	acgttagtat	cctgacacgg	1560
gccctgcaag	caaacttttc	tgattttgaa	aatctacgcg	ccaaatcgct	taagctcaac	1620
gcgacctag						1629

<210> 169

<211> 1629

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
Coding region without introns

<400> 169

atgctcaacg	ccgcggttgc	tgccccgcga	tgttttgtat	atcccactga	tcgcgcagca	60
atgcgcttgg	gctttgctct	tcgtctctcc	tctcctgcac	ctctcttctc	aacagcacct	120
ttccgctcgac	agttgcatgc	ttccggcgtc	cgatcaattg	aacctgttat	ctttcgaaat	180
agccttgaaa	agactcttga	ggctcatcga	tcctccaatc	gagccagtct	gatccgcaag	240
gtgattaacc	acgattgtcc	tgctgaaacg	ccccctccaa	ttttaccact	tgagaatcgt	300
gctggctcatg	atcaatcatc	tcaaaaggcc	tcctccgtgt	caaatgcaga	gtcagagtcc	360
ccccggtctt	ctgcgcctgc	gagacgagcg	cagaggaagg	cccgttcgcc	cagccaagta	420
gccaccccg	agccccagac	aacagaatat	ccacaactgc	aatggcatgc	agatgaaacc	480
aagggccgac	cggcacaaa	tccttggtg	aagtacttga	ctaccgattg	gaaaacgccc	540
gatgccgttt	cgcgtctcga	cgcggagatc	cgcgctcttg	agctctacat	gacaccgacc	600
ccgtcggagc	ggactgagat	agatcggctg	gttgcaagata	tgggtagggt	gctagcggga	660
atcgtcccca	gcccccccca	ggtaaccggt	tcattggcga	cgcgatttgc	cttgagccac	720
tcgggtctcg	attttgtctt	acctgtccc	gattcagacc	gatccaccgc	tgacgttcgc	780

```

aagccgagtg ccacacggcc caaggtgctc cagacttaca aaaagctctt acatgaagtg      840
ggacatgcgc ttcagcagtc cccctcgttc gcggagcgag tccgcatcat aggcagccgt      900
ttcccgtcc tctcagccat ccatcgcccc acggggccgcc tgctgcagtt cactgcggt      960
gaagggctac cggcctctgt cgaatacatc atggattacc aggccgagta tccctcgatc     1020
cggccgctct acgtgaccgc tcgcctgata ctggaggcgc ggggtaggta tggccgtact     1080
cagatgtcta ttgaatccga tgccctcgta atgcttctcg tggccttcct caaaatgaac     1140
cacgggctgt ttcagcggcc cgactgtctc ggcgagcagc tgatcgcggt tctgcgcgcc     1200
tacggcagcg atattgacct gaccaccacc ggtgtgtccg tcgatcccc cagttgggtc     1260
aatgctagta cgggtcaaacg cgccagcgcc ctgtacgcgc ccgatgatct acccgcgcat     1320
ctgcgcggcc agcgctccct catcagcctc aagagaacag cagccgccag acgcaatctg     1380
cctgccgccca gccggctgtg cgtgcaggac cccaccaatt acatgaatga tctggggccgc     1440
agctgcgtgc gtacgttgga actccagcac acgttctcgc ttgctcatga cgtctcggc     1500
gcaagtctca agcgctggga tgacagtga cggccgcgca acgttagtat cctgacacgg     1560
gccctgcaag caaacttttc tgattttgaa aatctacgcg ccaaatcgct taagctcaac     1620
gcgacctag                                     1629

```

<210> 170

<211> 542

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
Protein sequence

<400> 170

```

Met Leu Asn Ala Ala Val Ala Ala Pro Arg Cys Phe Val Tyr Pro Thr
1              5              10              15

```

```

Asp Arg Ala Ala Met Arg Leu Gly Phe Ala Leu Arg Leu Ser Ser Pro
          20              25              30

```

```

Ala Pro Leu Phe Ser Thr Ala Pro Phe Arg Arg Gln Leu His Ala Ser
          35              40              45

```

```

Gly Val Arg Ser Ile Glu Pro Val Ile Phe Arg Asn Ser Leu Glu Lys
50              55              60

```

```

Thr Leu Glu Ala His Arg Ser Ser Asn Arg Ala Ser Leu Ile Arg Lys
65              70              75              80

```

```

Val Ile Asn His Asp Cys Pro Ala Glu Thr Pro Pro Pro Ile Leu Pro
          85              90              95

```

```

Leu Glu Asn Arg Ala Gly His Asp Gln Ser Ser Gln Lys Ala Ser Ser
          100             105             110

```

```

Val Ser Asn Ala Glu Ser Glu Ser Pro Arg Ser Ser Ala Pro Ala Arg
          115             120             125

```

```

Arg Ala Gln Arg Lys Ala Arg Ser Pro Ser Gln Val Ala Thr Pro Gln
          130             135             140

```

```

Pro Gln Thr Thr Glu Tyr Pro Gln Leu Gln Trp His Ala Asp Glu Thr
145              150             155             160

```

```

Lys Gly Arg Pro Ala Gln Ser Pro Trp Leu Lys Tyr Leu Thr Thr Asp
          165              170             175

```

```

Trp Lys Thr Pro Asp Ala Val Ser Arg Leu Asp Ala Glu Ile Arg Ala

```


180					185					190					
Leu	Glu	Leu	Tyr	Met	Thr	Pro	Thr	Pro	Ser	Glu	Arg	Thr	Glu	Ile	Asp
		195					200					205			
Arg	Leu	Val	Ala	Asp	Met	Gly	Arg	Leu	Leu	Ala	Gly	Ile	Val	Pro	Ser
	210					215					220				
Pro	Pro	Gln	Val	Thr	Gly	Ser	Trp	Arg	Thr	Arg	Phe	Ala	Leu	Ser	His
225					230					235					240
Ser	Gly	Leu	Asp	Phe	Val	Leu	Pro	Val	Pro	Asp	Ser	Asp	Arg	Ser	Thr
				245					250					255	
Arg	Asp	Val	Arg	Lys	Pro	Ser	Ala	Thr	Arg	Pro	Lys	Val	Leu	Gln	Thr
			260					265					270		
Tyr	Lys	Lys	Leu	Leu	His	Glu	Val	Gly	His	Ala	Leu	Gln	Gln	Ser	Pro
		275					280					285			
Ser	Phe	Ala	Glu	Arg	Val	Arg	Ile	Ile	Gly	Ser	Arg	Phe	Pro	Val	Leu
	290					295					300				
Ser	Ala	Ile	His	Arg	Pro	Thr	Gly	Arg	Leu	Leu	Gln	Phe	His	Cys	Gly
305					310					315					320
Glu	Gly	Leu	Pro	Ala	Ser	Val	Glu	Tyr	Ile	Met	Asp	Tyr	Gln	Ala	Glu
				325					330					335	
Tyr	Pro	Ser	Ile	Arg	Pro	Leu	Tyr	Val	Thr	Ala	Arg	Leu	Ile	Leu	Glu
			340					345					350		
Ala	Arg	Gly	Arg	Tyr	Gly	Arg	Thr	Gln	Met	Ser	Ile	Glu	Ser	Asp	Ala
		355					360					365			
Leu	Val	Met	Leu	Leu	Val	Ala	Phe	Leu	Lys	Met	Asn	His	Gly	Arg	Phe
		370				375					380				
Gln	Arg	Pro	Asp	Cys	Leu	Gly	Glu	Gln	Leu	Ile	Ala	Phe	Leu	Arg	Ala
385					390					395					400
Tyr	Gly	Ser	Asp	Ile	Asp	Leu	Thr	Thr	Thr	Gly	Val	Ser	Val	Asp	Pro
				405					410					415	
Pro	Ser	Trp	Phe	Asn	Ala	Ser	Thr	Val	Lys	Arg	Ala	Ser	Ala	Leu	Tyr
			420					425					430		
Ala	Pro	Asp	Asp	Leu	Pro	Ala	His	Leu	Arg	Gly	Gln	Arg	Ser	Leu	Ile
		435					440					445			
Ser	Leu	Lys	Arg	Thr	Ala	Ala	Ala	Arg	Arg	Asn	Leu	Pro	Ala	Ala	Ser
		450				455					460				
Arg	Leu	Cys	Val	Gln	Asp	Pro	Thr	Asn	Tyr	Met	Asn	Asp	Leu	Gly	Arg
465					470					475					480
Ser	Cys	Val	Arg	Thr	Leu	Glu	Leu	Gln	His	Thr	Phe	Ser	Leu	Ala	His
				485					490					495	
Asp	Arg	Leu	Gly	Ala	Ser	Leu	Lys	Arg	Trp	Asp	Asp	Ser	Glu	Pro	Ala
			500					505					510		

Ala Asn Val Ser Ile Leu Thr Arg Ala Leu Gln Ala Asn Phe Ser Asp
 515 520 525

Phe Glu Asn Leu Arg Ala Lys Ser Leu Lys Leu Asn Ala Thr
 530 535 540

<210> 171
 <211> 1573
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381
 Genomic sequence containing 3' and 5'-ends and the coding region

<220>
 <223> misc_feature
 <223> (683)..(683)
 <223> n is a, c, g, or t

<400> 171
 tgggtgcttag ggacctgtga gtttgtgaca caaccacccc cggaaccagg gattctccac 60
 cgcgcccccg accgaccatt ttggacttgg ttagtaagct ccagtgacca gaaagcttac 120
 cagctagctt cacttgagat atcacaagat gctttggctg gcctgccacg aggtcttgct 180
 ccatgtcaac cagcaggatt cagtctctgc ctcatctcag tccaggcgag gtttctttgc 240
 tggatcttgc ggctgatgac cctcgcgatg tgggtgtccct gtccgacaag gaagcggtga 300
 ttttgcagct ctacaatcaa atccaggaac tggaaactgga aaaggcactt cttgaacaag 360
 gtacgcgtca aatttatatt ttttctaatt ttcttttttt tgtttctctg atgtagcttc 420
 ttgggcccctc caaatctgtc agcccagggt actgattccc actagagctg gaaccggctt 480
 ctggggacaa tctggatgag caacttgcaa tcgcagaacg tgagcttctc gaggcaaggg 540
 ccacgtacac ggtcaggaga aaggccacca gtactgtcct gatgactgat ccaacattaa 600
 aagctgttca cttgaaagct atatcacctg ttgaaagggt ttacctcctt tcagtttatg 660
 cgagcatttc aattctgcat tcncctatac taacgcttca tagagctctt ctacccttgg 720
 tcaaccggcg tgatgtgttg tctttggcac atgagaacct aatgaatgag cacaacgcga 780
 ctttgaggga actatccaat ttagaagtac aaaatctaga gctacaccag aggaatcaag 840
 agctagcgcg gcagcttctt gagtccgcga aggatgatga ttcatggaga gaagcactgg 900
 atgatgacga cctcaaggca caacttgagc agctagaggc cgatcgcaaa aagagcaaatt 960
 caagatggga agtcatgaaa agcgttgcaa gtgctattgt tgtgggaagt ggagtgaact 1020
 gggctgaaga cgatgagctt acagctctag tcattgatga atctgatgat taaataatcg 1080
 cctcgaaatt aatgatttctg aacaatttgg tagtattgac ttctccgacc ggcgtactac 1140
 aggatatgac ttccatttat gactagtaga gtaaacctca ttcatatttt ccaactaggg 1200
 cggatatata acagtatcgt cttggtcgaa tcagcagaac ggctgaggaa gctcgggttag 1260
 gtaccgtaag tgcgcccag actgccgata acctgaagac gcgccagcgc ccactagaac 1320
 aatcttcagt ggccgtgaga cccacgtgac atcatcgtcc atccacacta acaagacttg 1380
 actgtcagac catatgatatt ctgctgggtg tcccaaataa taatcttcat acatacatg 1440
 gccctgaagc cctggaatca tggagaaaat tcgaatacag atggaaggca attagaaccc 1500
 gataagggtg gcgctaattg atggatgcgt ctaagaatgt tatgcattaa tcagcgattt 1560
 acgggtaacc atg 1573

<210> 172
 <211> 573
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381
 Genomic sequence containing the coding region

<220>
 <223> misc_feature
 <223> (183)..(183)
 <223> n is a, c, g, or t

<400> 172
 caacttgcaa tcgcagaacg tgagcttctc gaggcaaggg ccacgtacac ggtcaggaga 60
 aaggccacca gtactgtcct gatgactgat ccaacattaa aagctgttca cttgaaagct 120
 atatcacctg ttgaaagggt ttacctcctt tcagtttatg cgagcatttc aattctgcat 180
 tcncctatac taacgcttca tagagctctt ctacccctgg tcaaccggcg tgatgtgttg 240
 tctttggcac atgagaacct aatgaatgcg cacaacgcga ctttgaggga actatccaat 300
 ttagaagtac aaaatctaga gctacaccag aggaatcaag agctagcgcg gcagcttctt 360
 gagtccgcga aggatgatga ttcattggaga gaagcactgg atgatgacga cctcaaggca 420
 caacttgagc agctagaggc cgatcgcaaa aagagcaaat caagatggga agtcatgaaa 480
 agcgttgcaa gtgctattgt tgtgggaagt ggagtgaact gggctgaaga cgatgagctt 540
 acagctctag tcattgatga atctgatgat taa 573

<210> 173
 <211> 573
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381
 Coding region without introns

<220>
 <223> misc_feature
 <223> (183)..(183)
 <223> n is a, c, g, or t

<400> 173
 caacttgcaa tcgcagaacg tgagcttctc gaggcaaggg ccacgtacac ggtcaggaga 60
 aaggccacca gtactgtcct gatgactgat ccaacattaa aagctgttca cttgaaagct 120
 atatcacctg ttgaaagggt ttacctcctt tcagtttatg cgagcatttc aattctgcat 180
 tcncctatac taacgcttca tagagctctt ctacccctgg tcaaccggcg tgatgtgttg 240
 tctttggcac atgagaacct aatgaatgcg cacaacgcga ctttgaggga actatccaat 300
 ttagaagtac aaaatctaga gctacaccag aggaatcaag agctagcgcg gcagcttctt 360
 gagtccgcga aggatgatga ttcattggaga gaagcactgg atgatgacga cctcaaggca 420
 caacttgagc agctagaggc cgatcgcaaa aagagcaaat caagatggga agtcatgaaa 480
 agcgttgcaa gtgctattgt tgtgggaagt ggagtgaact gggctgaaga cgatgagctt 540
 acagctctag tcattgatga atctgatgat taa 573

<210> 174
 <211> 190
 <212> PRT
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381
 Protein sequence

<400> 174

Gln Leu Ala Ile Ala Glu Arg Glu Leu Leu Glu Ala Arg Ala Thr Tyr
 1 5 10 15

Thr Val Arg Arg Lys Ala Thr Ser Thr Val Leu Met Thr Asp Pro Thr
 20 25 30

Leu Lys Ala Val His Leu Lys Ala Ile Ser Pro Val Glu Arg Phe Tyr
 35 40 45
 Leu Leu Ser Val Tyr Ala Ser Ile Ser Ile Leu His Ser Pro Ile Leu
 50 55 60
 Thr Leu His Arg Ala Leu Leu Pro Leu Val Asn Arg Arg Asp Val Leu
 65 70 75 80
 Ser Leu Ala His Glu Asn Leu Met Asn Ala His Asn Ala Thr Leu Arg
 85 90 95
 Glu Leu Ser Asn Leu Glu Val Gln Asn Leu Glu Leu His Gln Arg Asn
 100 105 110
 Gln Glu Leu Ala Arg Gln Leu Leu Glu Ser Ala Lys Asp Asp Asp Ser
 115 120 125
 Trp Arg Glu Ala Leu Asp Asp Asp Asp Leu Lys Ala Gln Leu Glu Gln
 130 135 140
 Leu Glu Ala Asp Arg Lys Lys Ser Lys Ser Arg Trp Glu Val Met Lys
 145 150 155 160
 Ser Val Ala Ser Ala Ile Val Val Gly Ser Gly Val Asn Trp Ala Glu
 165 170 175
 Asp Asp Glu Leu Thr Ala Leu Val Ile Asp Glu Ser Asp Asp
 180 185 190

<210> 175

<211> 2593

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 175

tgtcaaagaa	agtggatata	tatgctgctt	gttctcacct	ggtaatccat	cttgaatcac	60
gtccactaag	aatcagaaaa	actgagcgag	tggacaaaaa	cgggtgatac	gcatacgataa	120
gcttcgactg	gaaattcgga	gatacgccata	tatttgagtt	atgtaagcac	cgccgcaggc	180
gtctcattgg	gctggggaag	ctatcaacaa	ccaccagag	cttcttgaac	ttaactccgg	240
gggtgcatga	ctaatagttt	caataatgga	cgtcggatgc	tttgtaaatac	aacggcggtc	300
ctacaatggg	gatctatgca	cagttcggtt	cataggtaaa	gttgagggca	ccaccggcga	360
gtggctcgga	gtggaatggg	atgacccac	gcgggggaag	cattctggag	aacacaacgg	420
agtgaatat	tttacaatga	tgaagattt	ttcaagactg	gatagagcgg	attgactgac	480
ttgaacggaa	ggtagaagga	aacacccac	ggctgggttcg	ttcgtgcgcc	cttcgcgacg	540
gaccgacaga	cctcgaggct	tccttgaggc	agtgcgtcac	aagtatgctt	ctgagttcca	600
agaagaactc	gcaagacagc	agtcaggcga	agtctctgct	gcgcgggaaa	tcatcaaatt	660
tagtagcaaa	gtagtggaag	aggtcggctt	cgacaagatc	cggaagaaac	ttgcagagct	720
ccaggaattg	aaaatcgtgc	tcctggatcg	cctatgcatc	gcaggagttc	tcctcatag	780
agcgagtcta	catgagcttg	cagaggcttg	caaggagata	gaacagacat	gtcctaagat	840
cgttgacctc	gatctgagtt	acaacttact	ggaaagctgg	gttgacattg	caaacatatg	900
tcaacagctg	aagcgcttga	agacattgaa	gctgatgttg	gtcattcagt	acatctgtga	960
gaagcatgct	gacagttggc	agcggaaatc	gtctaggtcc	tcgacaggag	ggtctgatat	1020
tcgacggtat	cacaacacta	cacttgagcg	agactctact	cgaatgggac	gaggtatgct	1080
gcacaaagct	actgcttggg	taccagtgag	ctgactgact	cttggtcccc	tttagatttc	1140
agctttgaca	tatcaattcc	cgctactctc	tgctctgtct	gcctccgcaa	atcagattac	1200

ccagatcttg	acacctatca	cggataccat	cacgaccttg	acactggaaa	acaatgacat	1260
ctcttcgcta	tcttcattag	catgtctgac	ctctttgagc	aagctcgagc	acctctcgct	1320
gagagagaat	cgtatcgga	aagtctatgc	gtctggcatg	gaaggaaact	ctcttcagtt	1380
ttccgaaaat	ctcagatcgg	tggacctatc	cagaaacaat	atcgattctt	ggctgtttgt	1440
gaatgaactt	caacgcgtat	ttcttgggct	gcaatctttg	cgcatatcag	gaaatcccct	1500
gtacgacaag	cctgttgccc	cctcgaacgt	cacaaattta	ccggagaagc	caatgacggt	1560
ggacgaggcc	tatatgctaa	cactctctcg	actcgcttcc	atccaaacgc	tcaactacag	1620
caagataact	tcccaagacc	gaagtaatgg	cgaactctat	tacctttccc	tcattggcaa	1680
ggagttatcc	gcgtatccgg	aaagcgcaga	acgcgagatt	cttgctacac	atcccgccta	1740
tcaggagctt	tgtgagaaat	acggagcgcc	cacaatcagg	agagccgagc	tggcaggcgc	1800
tgccgtgaat	ccgcgctctg	ttgccgccc	agtagtgaag	ttggcttttt	gcttgcactc	1860
atcagttagt	tccggtgcaa	accaagaaca	atttcgagtt	cagaagatcc	cgagatcctt	1920
taatacatat	caagtcaagg	caatcgccctc	ccgcctgttc	aatttgccgc	cttaccagtg	1980
ccgactagtc	tgggagacca	acgagttaga	ccctattcat	caggagaaaa	aggacgatgg	2040
agacgattgg	gatagtgatg	aggatgaagc	cacagctatt	ggattggggg	agagtaacaa	2100
gctcacaccg	gcgacggagg	atggaaagtt	catcagaaga	gaggttgagc	tcctggattc	2160
aacgcgagac	ataggctttt	ggttccaacc	cgatactgtt	gaggcaagga	tcagagtaga	2220
agttgcaaca	tcgaattgac	aactatttcg	acataggagt	tgtgaaggag	ttccttaacc	2280
tacattgtcg	cgggtggggg	aatatatata	gttgagcacg	actcgtgcgt	taggatacaa	2340
cgaggtcaac	gacagaaaag	tagaacctct	tacgcaagcg	cctgtggcct	ctgttaccgc	2400
aatggattta	gaggccttct	tggttattct	taaacaatat	gatattgtgt	gtgtatattc	2460
aagctggagg	gcaacactga	ctgctgtttt	aggactaggt	cggttttggg	tggcagatta	2520
tcaccgcaac	tgttttgtga	taacagtgat	atcatttccc	tttcatataa	caatttaata	2580
ctcagacatc	gtc					2593

<210> 176

<211> 1974

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622
 Genomic sequence containing the coding region

<400> 176

atggacgtcg	gatgctttgt	aaatcaacgg	cggctcctaca	atgggggatct	atgcacagtt	60
cgttacatag	gtaaagtga	gggcaccacc	ggcgagtggc	tcggagtggg	atgggatgac	120
cccacgcggg	ggaagcattc	tggagaacac	aacggagtga	gatattttac	atgtatgaaa	180
gtattttcaa	gactggatag	agcggattga	ctgacttgaa	cggaaggtag	aaggaaacac	240
cccacggctg	gttcgttcgt	gcgcccttcg	cgacggaccg	acagacctcg	aggcttcctt	300
gaggcagtgc	gtcacaagta	tgcttctgag	ttccaagaag	aactcgcaag	acagcagtca	360
ggcgaagtct	ctgctgcgcg	ggaaatcatc	aaatttagta	gcaaaagtagt	ggaagaggtc	420
ggcttcgaca	agatccggaa	gaaacttgca	gagctccagg	aattgaaaat	cgtgctcctg	480
gatcgccat	gcacgcagg	agttctccct	catagagcga	gtctacatga	gcttgacagag	540
gcttgcaagg	agatagaaca	gacatgtcct	aagatcggtg	acctcgatct	gagttacaac	600
ttactggaaa	gctgggttga	cattgcaaac	atatgtcaac	agctgaagcg	cttgaagaca	660
ttgaagctga	tgttggtcat	tcagtacatc	tgtgagaagc	atgctgacag	ttggcagcgg	720
aaatcgtcta	ggtcctcgac	aggaggtct	gatattcgac	ggtatcacaa	cactacactt	780
ggacgagact	ctactcgaat	gggacgaggt	atgctgcaca	aagctactgc	ttggttacca	840
gtgagctgac	tgactcttgg	ttcccttttag	atttcagctt	tgacatatca	attcccgtca	900
ctctctgctc	tgtctgcctc	cgcaaatcag	attaccaga	tcttgacacc	tatcacggat	960
accatcacga	ccttgacact	ggaaaacaat	gacatctctt	cgctatcctc	attagcatgt	1020
ctgacctctt	tgaagaaagt	cgagcacctc	tcgctgagag	agaatcgtat	cgggaaagtc	1080
tatgcgtctg	gcatggaagg	aaactctctt	cagttttccg	aaaatctcag	atcgggtggac	1140
ctatccagaa	acaatatcga	ttcttggtcg	tttgtgaatg	aacttcaacg	cgtatttccct	1200
gggctgcaat	ctttgcgcac	atcaggaaat	cccctgtacg	acaagcctgt	tgccccctcg	1260
aacgtcacaa	atttaccgga	gaagccaatg	acggtggacg	aggcctatat	gctaacactc	1320
tctcgactcg	cttccatcca	aacgctcaac	tacagcaaga	taacttccca	agaccgaagt	1380
aatggcgaac	tctattacct	ttccctcatt	ggcaaggagt	tatccgcgta	tccggaaagc	1440
gcagaacgcg	agattcttgc	tacacatccc	cgctatcagg	agctttgtga	gaaatacggg	1500

```

gcgcccacaa tcaggagagc cgagctggca ggcgctgccg tgaatccgcg ctctgttgcc 1560
gcccagtag tagaagttggc tttttgcttg cactcatcag ttagttccgg tgcaaaccac 1620
gaacaatttc gagttcagaa gatcccagaa tcctttaata catatcaagt caaggcaatc 1680
gcctcccgcc tgttcaattt gccgccttac cagtgccgac tagtctggga gaccaacgag 1740
ttagacccta ttcacagga gaaaaaggac gatggagacg attgggatat tgatgaggat 1800
gaagccacag ctattggatt gggggagagt aacaagctca caccggcgac ggaggatgga 1860
aagttcatca gaagagaggt tgagctcctg gattcaacgc gagacatagg cttttggttc 1920
caaccgata ctgttgaggc aaggatcaga gtagaagttg caacatcgaa ttga 1974

```

<210> 177

<211> 1830

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622
Coding region without introns

<400> 177

```

atggacgtcg gatgctttgt aaatcaacgg cggtcctaca atggggatct atgcacagtt 60
cgttacatag gtaaagttga gggcaccacc ggcgagtggc tcggagtgga atgggatgac 120
cccacgcggg ggaagcattc tggagaacac aacggagtga gatattttac atgtagaagg 180
aaacacccca cggctggttc gttcgtgccc ccttcgcgac ggaccgacag acctcgaggc 240
ttccttgagg cagtgcgtca caagtatgct tctgagttcc aagaagaact cgcaagacag 300
cagtcaggcg aagtctctgc tgcgcgggaa atcatcaa attagtagcaa agtagtgga 360
gaggtcggct tcgacaagat ccggaagaaa cttgcagagc tccaggaatt gaaaatcgtg 420
ctcctggatc gcctatgcat cgcaggagtt ctccctcata gagcaggtct acatgagctt 480
gcagaggctt gcaaggagat agaacagaca tgtcctaaga tcgttgacct cgatctgagt 540
tacaacttac tggaaagctg ggttgacatt gcaaacatat gtcaacagct gaagcgcttg 600
aagacattga agctgatgtt ggtcattcag tacatctgtg agaagcatgc tgacagttgg 660
cagcggaat cgtctaggct ctcgacagga gggctctgata ttcgacggta tcacaacact 720
acacttgagc gagactctac tcgaatggga cgaggtatgc tgcacaaagc tactgcttgg 780
ttaccaatta cccagatctt gacacctatc acggatacca tcacgacctt gacactggaa 840
aacaatgaca tctcttcgct atcctcatta gcatgtctga cctctttgag caagctcgag 900
cacctctcgc tgagagagaa tcgtatcggg aaagtctatg cgtctggcat ggaaggaaac 960
tctcttcagt tttccgaaaa tctcagatcg gtggacctat ccagaaacaa tatcgattct 1020
tggtctgttg tgaatgaact tcaacgcgta tttcctgggc tgcaatcttt gcgcatatca 1080
ggaaatcccc tgtacgacaa gcctgttgcc ccctcgaacg tcacaaatth accggagaag 1140
ccaatgacgg tggacgaggg ctatatgcta acactctctc gactcgcttc catccaaacg 1200
ctcaactaca gcaagataac ttcccaagac cgaagtaatg gcgaactcta ttacctttcc 1260
ctcattggca aggagttatc cgcgtatccg gaaagcgcag aacgcgagat tcttgctaca 1320
catccccgct atcaggagct ttgtgagaaa tacggagcgc ccacaatcag gagagccgag 1380
ctggcaggcg ctgccgtgaa tccgcgctct gttgccgccc gagtagtgaa gttggctttt 1440
tgcttgcaat catcagttag ttccggtgca aaccaagaac aatttctgagt tcagaagatc 1500
ccgagatcct ttaatacata tcaagtcaag gcaatcgctt cccgcctgtt caatttgccg 1560
ccttaccagt gccgactagt ctgggagacc aacgagttag accctattca tcaggagaaa 1620
aaggacgatg gagacgattg ggatagtgat gaggatgaag ccacagctat tggattgggg 1680
gagagtaaca agctcacacc ggcgacggag gatggaaagt tcatcagaag agaggttgag 1740
ctcctggatt caacgcgaga cataggcttt tggttccaac ccgatactgt tgaggcaagg 1800
atcagagtag aagttgcaac atcgaattga

```

<210> 178

<211> 609

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622

Protein sequence

<400> 178

```

Met Asp Val Gly Cys Phe Val Asn Gln Arg Arg Ser Tyr Asn Gly Asp
1          5          10          15
Leu Cys Thr Val Arg Tyr Ile Gly Lys Val Glu Gly Thr Thr Gly Glu
20          25          30
Trp Leu Gly Val Glu Trp Asp Asp Pro Thr Arg Gly Lys His Ser Gly
35          40          45
Glu His Asn Gly Val Arg Tyr Phe Thr Cys Arg Arg Lys His Pro Thr
50          55          60
Ala Gly Ser Phe Val Arg Pro Ser Arg Arg Thr Asp Arg Pro Arg Gly
65          70          75          80
Phe Leu Glu Ala Val Arg His Lys Tyr Ala Ser Glu Phe Gln Glu Glu
85          90          95
Leu Ala Arg Gln Gln Ser Gly Glu Val Ser Ala Ala Arg Glu Ile Ile
100         105         110
Lys Phe Ser Ser Lys Val Val Glu Glu Val Gly Phe Asp Lys Ile Arg
115         120         125
Lys Lys Leu Ala Glu Leu Gln Glu Leu Lys Ile Val Leu Leu Asp Arg
130         135         140
Leu Cys Ile Ala Gly Val Leu Pro His Arg Ala Ser Leu His Glu Leu
145         150         155         160
Ala Glu Ala Cys Lys Glu Ile Glu Gln Thr Cys Pro Lys Ile Val Asp
165         170         175
Leu Asp Leu Ser Tyr Asn Leu Leu Glu Ser Trp Val Asp Ile Ala Asn
180         185         190
Ile Cys Gln Gln Leu Lys Arg Leu Lys Thr Leu Lys Leu Met Leu Val
195         200         205
Ile Gln Tyr Ile Cys Glu Lys His Ala Asp Ser Trp Gln Arg Lys Ser
210         215         220
Ser Arg Ser Ser Thr Gly Gly Ser Asp Ile Arg Arg Tyr His Asn Thr
225         230         235         240
Thr Leu Gly Arg Asp Ser Thr Arg Met Gly Arg Gly Met Leu His Lys
245         250         255
Ala Thr Ala Trp Leu Pro Ile Thr Gln Ile Leu Thr Pro Ile Thr Asp
260         265         270
Thr Ile Thr Thr Leu Thr Leu Glu Asn Asn Asp Ile Ser Ser Leu Ser
275         280         285
Ser Leu Ala Cys Leu Thr Ser Leu Ser Lys Leu Glu His Leu Ser Leu
290         295         300

```

Arg Glu Asn Arg Ile Gly Lys Val Tyr Ala Ser Gly Met Glu Gly Asn
 305 310 315 320
 Ser Leu Gln Phe Ser Glu Asn Leu Arg Ser Val Asp Leu Ser Arg Asn
 325 330 335
 Asn Ile Asp Ser Trp Leu Phe Val Asn Glu Leu Gln Arg Val Phe Pro
 340 345 350
 Gly Leu Gln Ser Leu Arg Ile Ser Gly Asn Pro Leu Tyr Asp Lys Pro
 355 360 365
 Val Ala Pro Ser Asn Val Thr Asn Leu Pro Glu Lys Pro Met Thr Val
 370 375 380
 Asp Glu Ala Tyr Met Leu Thr Leu Ser Arg Leu Ala Ser Ile Gln Thr
 385 390 395 400
 Leu Asn Tyr Ser Lys Ile Thr Ser Gln Asp Arg Ser Asn Gly Glu Leu
 405 410 415
 Tyr Tyr Leu Ser Leu Ile Gly Lys Glu Leu Ser Ala Tyr Pro Glu Ser
 420 425 430
 Ala Glu Arg Glu Ile Leu Ala Thr His Pro Arg Tyr Gln Glu Leu Cys
 435 440 445
 Glu Lys Tyr Gly Ala Pro Thr Ile Arg Arg Ala Glu Leu Ala Gly Ala
 450 455 460
 Ala Val Asn Pro Arg Ser Val Ala Ala Arg Val Val Lys Leu Ala Phe
 465 470 475 480
 Cys Leu His Ser Ser Val Ser Ser Gly Ala Asn Gln Glu Gln Phe Arg
 485 490 495
 Val Gln Lys Ile Pro Arg Ser Phe Asn Thr Tyr Gln Val Lys Ala Ile
 500 505 510
 Ala Ser Arg Leu Phe Asn Leu Pro Pro Tyr Gln Cys Arg Leu Val Trp
 515 520 525
 Glu Thr Asn Glu Leu Asp Pro Ile His Gln Glu Lys Lys Asp Asp Gly
 530 535 540
 Asp Asp Trp Asp Ser Asp Glu Asp Glu Ala Thr Ala Ile Gly Leu Gly
 545 550 555 560
 Glu Ser Asn Lys Leu Thr Pro Ala Thr Glu Asp Gly Lys Phe Ile Arg
 565 570 575
 Arg Glu Val Glu Leu Leu Asp Ser Thr Arg Asp Ile Gly Phe Trp Phe
 580 585 590
 Gln Pro Asp Thr Val Glu Ala Arg Ile Arg Val Glu Val Ala Thr Ser
 595 600 605
 Asn

<210> 179

<211> 1867

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 179

caactatttc	gacataggag	ttgtgaagga	gttccttaac	ctacattgtc	gcgggtgggg	60
taatatatat	agttgagcac	gactcgtgcg	ttaggataca	acgaggtcaa	cgacagaaaa	120
gtagaacctc	ttacgcaagc	gcctgtggcc	tctgttacct	gaatggattt	agaggccttc	180
ttggttattc	ttaaacaata	tgatatgtgt	agtgtatatt	caagctggag	ggcaaacactg	240
actgctgttt	taggactagg	tcggtttttg	gtggcagatt	atcaccgcaa	ctgtttttgtg	300
ataacagtga	tatcattttc	ctttcatata	acaattttaat	actcagacat	cgtcattggca	360
gaatactgga	aatcagctgt	aagtgccttt	cattcagttc	cgagacttc	ttcgtgataa	420
tctttacgtg	gggaagtccg	gcatcaactg	acagcaatat	tctagccccg	gttctggtgc	480
aaacaatgca	agatattcat	tcgggataca	cccttcgaga	aaaccagca	tgaagcgagt	540
gccaaacacc	agggaaacct	taagcgtttc	ctacgagata	tccaccggga	aaatgaacgg	600
aagcaaaagag	aaactcagaa	ggcgaaaggat	gaagtgcagc	gattaaggca	aactgtcgca	660
ggaaaaccag	gtgcaaaaga	cagcggcgca	acagcttggg	aacacgcctc	ggctgcccct	720
ccaccggcag	aacgacctgt	gtccctggaa	gagagaaaga	agcagatagc	gcagctggca	780
gagatgggaa	ttgctatccc	ggacgaatac	cgtggtgaac	tcgcgctcgc	tggcgaatgg	840
cagacgggat	ccgaacgagt	tattcgacca	gatgacgata	cagaggaagg	aaagcctggt	900
agctctatcg	gcgttcggaa	acgcaagatg	gaaggcgatg	aggaggagca	ggaggcgcg	960
caggaggccg	agagattcgt	gagtcagggt	tggggctcga	ggactcggca	gtatcctggg	1020
gagcagagcg	atgcagacct	ggatgcactt	ctaaattcta	ccaaggatgt	aaagaaggtc	1080
aagttgtcgg	cgccggatga	agggtcgaaa	gagaaggcta	gcaaagaggg	tgctacacca	1140
agcaacgata	cggaaccagg	tgccgctcag	gagtcagaac	taccatcagt	caagtctgag	1200
ggtaaaagaag	cggcgcagct	tgctacaaca	gataccccag	cggtgaagca	ggaagaggag	1260
gcggcaccta	caggagttgt	ttttaagaag	cgcaagccga	aggtcctgag	gaaatagtcg	1320
aattttgcagc	tgctggatat	ctattatcta	ccatgcgcac	aaatgtacag	atgatgcggt	1380
atggttgccg	acgggtccaat	atgcctcgcc	tgccggtgct	cacatgaagc	gatcatgggt	1440
tcttgtctca	ctgcgctcca	gtgttcgaaa	accgggatga	tgccctctggc	ctccagtcgt	1500
ccgtcgccga	agcaaccagc	ctcatagaag	atctggattc	tcgattcgct	tgccgagaaa	1560
gcctagtctg	gtcttgcggt	agcctatata	cagattgagt	gtatcgattc	gagcttatgc	1620
gggttgctctg	ataatattct	gccttacatt	ggcagagaga	cggttgagca	catagggtgg	1680
atggagaatg	atcagttctt	acgtatgtaa	gcatgatgtc	tagctcagaa	aagagtccca	1740
tataccatgc	gactcgttgg	cagcatccac	ctcttccttt	ggagtgcgat	ctacaatagc	1800
atgcatacga	aacaaatttc	gttgacaagg	agaccagggg	cgagaagagt	aatatagcaa	1860
gccagct						1867

<210> 180

<211> 963

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135
 Genomic sequence containing the coding region

<400> 180

atggcagaat	actggaaatc	agctgtaagt	gcccttcatt	cagttccgca	gacttcttcg	60
tgataatctt	tacgtgggga	agtccggcat	caactgacag	caatattcta	gccccgggtc	120
tggtgcaaac	aatgcaagat	attcattcgg	gatacacctt	tcgagaaaac	ccagcatgaa	180
gcgagtgcc	aacaccagg	aaaccttaag	cgtttcctac	gagatatcca	ccgggaaaat	240
gaacggaagc	aaagagaaac	tcagaaggcg	aaggatgaag	tcgagcgatt	aaggcaaaact	300
gtcgcaggaa	aaccaggtgc	aaaagacagc	ggcgcaacag	cttggaaca	cgctcgggt	360
gcccctccac	cggcagaacg	acctgtgtcc	ctggaagaga	gaaagaagca	gatagcgag	420
ctggcagaga	tgggaattgc	tatcccggac	gaataaccgtg	gtgaactcgc	gctcgtggc	480

```

gaatggcaga cggatatccga acgagttatt cgaccagatg acgatacaga ggaaggaaag 540
cctggtagct ctatcggcgt tcggaaacgc aagatggaag gcgatgagga ggagcaggag 600
gcgcgacagg aggccgagag attcgtgagt caggggttggg gctcgaggac tcggcagtat 660
cctggggagc agagcgatgc agacctggat gcacttctaa attctaccaa ggatgtaaag 720
aaggtcaagt tgtcggcgcc ggatgaaggg tcgaaagaga aggctagcaa agaggggtgct 780
acaccaagca acgatacggg ccaggctgcg gctcaggagt cagaactacc atcagtcaag 840
tctgagggta aagaagcggc gcagcttgct acaacagata cccagcggt gaagcaggaa 900
gaggaggcgg cacctacagg agttgttttt aagaagcgca agccgaaggt cctgaggaaa 960
tag

```

<210> 181

<211> 876

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135
Coding region without introns

<400> 181

```

atggcagaat actggaaatc agctccccgg ttctggtgca aacaatgcaa gatattcatt 60
cgggatacac ccttcgagaa aaccagcat gaagcgagt ccaaacacca gggaaacctt 120
aagcggtttcc tacgagatat ccaccgggaa aatgaacgga agcaaagaga aactcagaag 180
gcgaaggatg aagtcgagcg attaaggcaa actgtcgag gaaaaccagg tgcaaaagac 240
agcggcgcaa cagcttggaa acacgcctcg gctgcccctc caccggcaga acgacctgtg 300
tccctggaag agagaaagaa gcagatagcg cagctggcag agatgggaat tgctatcccg 360
gacgaatacc gtggtgaact cgcgctcgct ggcgaatggc agacggtatc cgaacgagtt 420
attcgaccag atgacgatac agaggaagga aagcctggta gctctatcgg cgttcggaaa 480
cgcaagatgg aaggcgatga ggaggagcag gaggcgcgac aggaggccga gagattcgtg 540
agtcagggtt ggggctcgag gactcggcag tctcctgggg agcagagcga tgcagacctg 600
gatgcacttc taaattctac caaggatgta aagaaggtca agttgtcggc gccggatgaa 660
gggtcgaaaag agaaggctag caaagagggt gctacaccaa gcaacgatac ggaccaggct 720
gcggtcagg agtcagaact accatcagtc aagtctgagg gtaaaagaagc ggcgagctt 780
gctacaacag ataccccagc ggtgaagcag gaagaggagg cggcacctac aggagtgtt 840
ttaaagaagc gcaagccgaa ggtcctgagg aaatag 876

```

<210> 182

<211> 291

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135
Protein sequence

<400> 182

```

Met Ala Glu Tyr Trp Lys Ser Ala Pro Arg Phe Trp Cys Lys Gln Cys
1           5           10           15

Lys Ile Phe Ile Arg Asp Thr Pro Phe Glu Lys Thr Gln His Glu Ala
20           25           30

Ser Ala Lys His Gln Gly Asn Leu Lys Arg Phe Leu Arg Asp Ile His
35           40           45

Arg Glu Asn Glu Arg Lys Gln Arg Glu Thr Gln Lys Ala Lys Asp Glu
50           55           60

```

Val Glu Arg Leu Arg Gln Thr Val Ala Gly Lys Pro Gly Ala Lys Asp
 65 70 75 80
 Ser Gly Ala Thr Ala Trp Lys His Ala Ser Ala Ala Pro Pro Pro Ala
 85 90 95
 Glu Arg Pro Val Ser Leu Glu Glu Arg Lys Lys Gln Ile Ala Gln Leu
 100 105 110
 Ala Glu Met Gly Ile Ala Ile Pro Asp Glu Tyr Arg Gly Glu Leu Ala
 115 120 125
 Leu Ala Gly Glu Trp Gln Thr Val Ser Glu Arg Val Ile Arg Pro Asp
 130 135 140
 Asp Asp Thr Glu Glu Gly Lys Pro Gly Ser Ser Ile Gly Val Arg Lys
 145 150 155 160
 Arg Lys Met Glu Gly Asp Glu Glu Glu Gln Glu Ala Arg Gln Glu Ala
 165 170 175
 Glu Arg Phe Val Ser Gln Gly Trp Gly Ser Arg Thr Arg Gln Tyr Pro
 180 185 190
 Gly Glu Gln Ser Asp Ala Asp Leu Asp Ala Leu Leu Asn Ser Thr Lys
 195 200 205
 Asp Val Lys Lys Val Lys Leu Ser Ala Pro Asp Glu Gly Ser Lys Glu
 210 215 220
 Lys Ala Ser Lys Glu Gly Ala Thr Pro Ser Asn Asp Thr Asp Gln Ala
 225 230 235 240
 Ala Ala Gln Glu Ser Glu Leu Pro Ser Val Lys Ser Glu Gly Lys Glu
 245 250 255
 Ala Ala Gln Leu Ala Thr Thr Asp Thr Pro Ala Val Lys Gln Glu Glu
 260 265 270
 Glu Ala Ala Pro Thr Gly Val Val Phe Lys Lys Arg Lys Pro Lys Val
 275 280 285
 Leu Arg Lys
 290

<210> 183

<211> 2193

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 183

gagcaactgc	cagaaatcca	gacgtgcaac	tcctccgcaa	aaaaaagcgt	tgtctcccaa	60
aacggaggct	gttaagttat	cgccacgggg	aaatagccca	aaaggaactc	gtcacagctg	120
gaatcaacac	caagtaccga	agaaacaagc	gagcagcggc	tgtttggtt	ctgcagctgc	180
acaaaaaatg	ggaacgaagt	gaatgaggtt	agatagagat	gaggatggat	caagaagcgc	240
cctccagatg	tagcaatgaa	gagatgatgt	tgcaagaaga	ggtgaaacaa	gctggcggca	300

cgggatcagg	ctaggctaga	taggggttagc	aacgaggggtg	acatcacgtg	agaacgggca	360
tcgtgatatg	gatgacaatt	aacatcataa	acactcttcg	ttcagttgct	gtgactcctg	420
acgcgtaagg	ggatctgggg	tgaagtcaag	caatagactc	tctgacagat	ttgactttag	480
agaaaagtaaa	taacaccact	atggacatct	cgcaagaaac	cgttgataaa	atacgacgtt	540
tcgcgcacaaa	gcgcacaaaa	gcggaggagt	tctacgagga	acactcggta	aatccagcta	600
attttgacgc	ttacaatcgc	aagttggatg	agacgttggc	agagctgcag	gctcaagtca	660
aacgtcatga	ggatgagctc	cgcaaggtag	gtcaacaagt	tgcctagaat	ataagccgac	720
tgtcacaaga	gatttcatgc	atgaattagg	aatactgaca	agaggaacag	ctacgcatga	780
ccaccacgat	cgagttcgct	caaattgggg	cagatccttg	ggcccgcac	tcagaagtgc	840
gcagagccaa	gaaagcgtat	gattctcttc	tgcaatcgga	aacgcgactg	ccgagtcag	900
gctcgccctt	gccttcatta	cttgcggttg	acgaggcgct	tcgtctcgct	aaggagagca	960
agacctcaat	ctcactgacg	gcggagaaac	tgtctgcgga	tcgtcagcgc	ttgaaagcgg	1020
aagaagccaa	tttgcgcgat	gcgcaactga	tcaaagacgg	gttggagaaa	aggattgagc	1080
ggctgaacgc	agaaaaatcg	agtcaagtcc	agaaaactcc	tgcgacagct	gcgtatgatc	1140
tcgtcaagga	gcagcaggaa	aagatcgaga	gacttgatac	taccacagaa	gagctaaagt	1200
cctctctcta	taaatttgct	gaagacacac	ttgcccacat	gcttgctgca	gaaaatctgg	1260
gcggtcccac	tgtcggagat	gcgttggaac	tttcggacac	taccttaaaa	gcgggctaca	1320
ctagccatgg	gaagcctaag	aaacccaaaa	ctccggccgt	ggggacttct	gacagtggcc	1380
aacagcggat	tgacgagctt	gttcgtcgcc	aaactgcgca	ggagggcaac	gagcaggcaa	1440
cccttttgaa	caaaagagag	gcggccgcgc	ctgaaatgcg	agctcttctt	actgctctgt	1500
tagatgcgga	ttactcctat	gtcgaccttc	cgacagagtc	agcggcctcg	cgctttctag	1560
taagagcgaa	ggtagctcaa	ttccatccgc	gcgatgccag	gaagcttcgg	ttaattgatt	1620
ttgggcgctc	attagtcgat	tgaggtggct	acatgtaccg	tactacatct	cccagcttac	1680
aatggtatc	acatttcacc	aaacatctgg	gaaaagacaa	acagacgcca	tccccacgga	1740
tatatagcga	ctcaaccgaa	agccagtaag	atatctagag	ccggcgaaaa	ccacgtgttt	1800
caacgaagaa	gcggccccga	aagccactgg	tagcataacg	ccttgagaat	gcgagagata	1860
catcaaaagc	ttatcagaaa	gttcaatgct	cgaggtcaaa	aatataccgt	taatgccata	1920
caagaaacat	ggaagaagaa	agaccgtagc	cggttatcag	atcggcatca	ttccgatgct	1980
ggtagaagta	ctcttgccgc	tattctttgc	tttgagacca	gttcgggaac	ccgccgagcg	2040
cttggtgact	tgatcgctgg	gctcccttct	aggtcgcggc	gtttttattt	ttgaactcga	2100
ccctgtagcg	ttcttgccgt	ggaagcgctt	cttgagcga	gtctttcttt	tcttggaacg	2160
gctagtctcg	gtgtcttcat	actcttcgga	tga			2193

<210> 184

<211> 1448

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663
Genomic sequence containing the coding region

<400> 184

atgtctgctt	ctccatccgc	actgcaatcg	accaagcggc	ccttgaggga	cccttcttcg	60
ccgtccggac	caaatgatca	gccagaagct	aaacgtcctg	ccttgagcaa	agtagtaaag	120
ggaaacgagt	cggagaccta	tacggatgcc	aaggctgagc	cttccgctgc	gccaagtgc	180
actgctgatg	gccaggcgga	cactgttggt	cctgatgctc	caaatggtaa	gggtgcatcc	240
acggagacgc	agccaattca	gtcgaccgcg	tctcatggcg	agcgcgtac	ttctcagccc	300
gaacagcagc	gcccacaaga	tgaatccagc	tggattcaca	ttcgcgctgt	aatttctagc	360
caggaagctg	ccacagtcac	tggcaagggt	ggagaaaacg	tatctcagat	tcgtcgtttg	420
tctggagcaa	agtgcactgt	cagcgactac	tcccggtgtg	cagtcgaacg	tattttgacc	480
gtgagcggcc	cacaggatgc	cgttgccaag	gttggttttt	tgatctatcc	ttcgctgttt	540
gaaagattgc	taattcagag	taggcggttg	gtttgatcat	ccgtacattg	aacaatgaac	600
ctcttgatgc	cccctctacc	gcccattcca	agacataccc	tctgcgtttg	ctgatcccc	660
atctccttat	tggctccatc	attggcaaag	gtggttcacg	cattcgcgaa	attcaggaag	720
cttctggtgc	cogactgaat	gcacccgatt	cgtgccttcc	cttgtcctct	gagcggtcac	780
ttgtaattct	cggcgttgcc	gattctgtcc	acatcgctac	ctaactacgt	gccgtaaccc	840
tcgttgagca	gctcactgag	cgctttggag	gtcctgcagc	ctcagcttat	gccactcgca	900
gcggtggccc	tgctggagca	gtgcctggcg	gtatgcaggt	tgtcccgtat	gttccacagc	960
ccgctggtgg	tcaatatggc	catccagaac	atttcaagag	acaccatcac	caccccaatc	1020

```

gcgctgctgc aggcgcctat ggggtccctt accttcacgg tcagcctgct cccgcaccag 1080
tggcccagcc ggctttgcat tatggagctg ctccccatgc cccttacgca ggagctggcc 1140
cccatcagcc tgctccatac ggcgcaccgc agcccgtcga ggcacgcggc gctcctaccc 1200
ctgccacacc cgttggaggt gtcatgcctg gtcagccatt gactcagcag atctacatcc 1260
ccaacgacat ggttgggtgcc atcatcggaa agggcggtgc gaagatcaat gagattcgac 1320
acctcagtg cagtgtgatc aagattaatg agcctcaaga gaacagcaat gagcgtttg 1380
tgactattac tggaacccag gaatgcaacc aaatggctct gtacatgctt tactcgcgac 1440
ttggttag

```

<210> 185

<211> 1395

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663
Coding region without introns

<400> 185

```

atgtctgctt ctccatccgc actgcaatcg accaagcggc ccttggagga cccttcttcg 60
ccgtccggac caaatgatca gccagaagct aaacgtcctg ccttggacaa agtagtaaag 120
ggaaacgagt cggagaccta tacggatgcc aaggctgagc cttccgctgc gccaagtgtc 180
actgctgatg gccagggcga cactgttggt cctgatgctc caaatggtaa ggggtgcatcc 240
acggagacgc agccaattca gtcgaccgcg tctcatggcg agcgcgtac ttctcagccc 300
gaacagcagc gccacaaga tgaatccagc tggattcaca ttcgcgctgt aatttctagc 360
caggaagctg ccacagtcac tggcaagggt ggagaaaacg tatctcagat tcgtcgtttg 420
tctggagcaa agtgactgt cagcgactac tcccggtgtg cagtcgaacg tattttgacc 480
gtgagcggcc cacaggatgc cgttgccaa gcgtttggtt tgatcatccg tacattgaac 540
aatgaacctc ttgatgcccc ctctaccgcc caatccaaga cataccctct gcgtttgctg 600
atcccccatc tccttatttg ctccatcatt ggcaaagggt gttcacgcac tcgcgaaatt 660
caggaagctt ctgggtgccc actgaatgca tccgattogt gccttccctt gtccctctgag 720
cggtcacttg taattctcgg cgttgccgat tctgtccaca tcgctacctc ctacgtcgcc 780
gtaaccctcg ttgagcagct cactgagcgc tttggaggtc ctgcagcctc agcttatgcc 840
actcgcagcg gtggccctgc tggagcagtg cctggcggtg tgcaggttgt cccgtatgtt 900
ccacagcccg ctggtgttca atatggccat ccagaacatt tcaagagaca ccatcaccac 960
cccaatcgcg ctgctgcagg cgctatggg gtcccttacc ttcacggtca gcctgtctcc 1020
gcaccagtgg cccagccggc tttgcattat ggagctgctc cccatgcccc ttacgcagga 1080
gctggcccc atcagcctgc tccatacggc gcaccgcagc ccgctcaggc acgcggcgct 1140
cctacccctg ccacaccctg tggaggtgtc atgcctggtc agccattgac tcagcagatc 1200
tacatcccca acgacatggt tggtgccatc atcggaaagg gcggtgcgaa gatcaatgag 1260
attcgacacc tcagtggcag tgtgatcaag attaatgagc ctcaagagaa cagcaatgag 1320
cgtttggtga ctattactg aaccaggaa tgcaaccaa tggctctgta catgctttac 1380
tcgcgacttg gttag

```

<210> 186

<211> 464

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663
Protein sequence

<400> 186

```

Met Ser Ala Ser Pro Ser Ala Leu Gln Ser Thr Lys Arg Pro Leu Glu
1           5           10           15

```

```

Asp Pro Ser Ser Pro Ser Gly Pro Asn Asp Gln Pro Glu Ala Lys Arg

```

154/169

Ala Pro His Ala Pro Tyr Ala Gly Ala Gly Pro His Gln Pro Ala Pro
 355 360 365

Tyr Gly Ala Pro Gln Pro Ala Gln Ala Arg Gly Ala Pro Thr Pro Ala
 370 375 380

Thr Pro Val Gly Gly Val Met Pro Gly Gln Pro Leu Thr Gln Gln Ile
 385 390 395 400

Tyr Ile Pro Asn Asp Met Val Gly Ala Ile Ile Gly Lys Gly Gly Ala
 405 410 415

Lys Ile Asn Glu Ile Arg His Leu Ser Gly Ser Val Ile Lys Ile Asn
 420 425 430

Glu Pro Gln Glu Asn Ser Asn Glu Arg Leu Val Thr Ile Thr Gly Thr
 435 440 445

Gln Glu Cys Asn Gln Met Ala Leu Tyr Met Leu Tyr Ser Arg Leu Gly
 450 455 460

<210> 187

<211> 2121

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 187

taagttatcg	ccacgggggaa	atagcccaaa	aggaactcgt	cacagctgga	atcaacacca	60
agtaccgaag	aaacaagcga	gcagcggtcg	tttggcttct	gcagctgcac	aaaaaatggg	120
aacgaagtga	atgaggttag	atagagatga	ggatggatca	agaagcgccc	tccagatgta	180
gcaatgaaga	gatgatgttg	caagaagagg	tgaaacaagc	tggcggcacg	ggatcaggct	240
aggctagata	gggttagcaa	cgagggtgac	atcacgtgag	aacgggcac	gtgatatgga	300
tgacaattaa	catcataaac	actcttcgtt	cagttgctgt	gactcctgac	gcgtaagggg	360
atctgggggtg	aagtcaagca	atagactctc	tgacagattt	gacttttagag	aaagtaaata	420
acaccactat	ggacatctcg	caagaaaccg	ttgataaaat	acgacgtttc	gcgcaaaagc	480
gccaaaaagc	ggaggagttc	tacgaggaac	actcggtaaa	tccagctaata	tttgacgctt	540
acaatcgcaa	gttggtgatg	acgttggcag	agctgcaggc	tcaagtcaaa	cgatcatgag	600
atgagctccg	caaggtacgt	caacaagttg	cctagaatat	aagccgactg	tcacaagaga	660
tttcatgcat	gaattaggaa	tactgacaag	aggaacagct	acgcatgacc	accacgatcg	720
agttcgctca	aattggggca	gatccttggg	cccgcatctc	agaagtgcgc	agagccaaga	780
aagcgataga	ttctcttctg	caatcggaag	cgcgactgcc	gagtcaggcg	tcgcccctgc	840
cttcattact	tgcggttgac	gaggcgtctc	gtctcgtcaa	ggagagcaag	acctcaatct	900
cactgacggc	ggagaaaactg	tctgcggatc	gtcagcgctt	gaaagcggaa	gaagccaatt	960
tgcgcgatgc	gcaactgatc	aaagacgggt	tgagagaaaag	gattgagcgg	ctgaacgcag	1020
aaaaatcgag	tcaagtccag	aaaactcctg	cgcagcttgc	gtatgatctc	gtcaaggagc	1080
agcaggaaaa	gatcgagaga	cttgataacta	ccacagaaga	gctaaagtcc	tctctctata	1140
aatttgctga	agacacactt	gccccaatgc	ttgctgcaga	aaatctgggc	ggtcccactg	1200
tcggagatgc	gttggaat	tcggacacta	ccctaaaagc	gggctacact	agccatggga	1260
agcctaagaa	accaaaaact	ccggccgtgg	ggacttctga	cagtggccaa	cagcggattg	1320
acgagcttgt	tcgtcgccaa	actgcgcagg	agggcaacga	gcaggcaacc	cttttgaaca	1380
aaagagaggc	ggccgcgct	gaaatgcgag	ctcttcttac	tgctctgtta	gatgcggatt	1440
actcctatgt	cgaccttccg	cacgagtcag	cggcctcgcg	ctttctagta	agagcgaagg	1500
tagctcaatt	ccatccgcgc	gatgccagga	agcttcgggt	aattgatttt	gggcgctcat	1560
tagtcgattg	aggtggctac	atgtaccgta	ctacatctcc	cagcttacaa	atggtatcac	1620
atttcaccaa	acatctggga	aaagacaaac	agacgccatc	cccacggata	tatagcgact	1680
caaccgaaag	ccagtaagat	atctagagcc	ggcgaaaacc	acgtgtttca	acgaagaagc	1740

```

ggccccgaaa gccactggta gcataacgcc ttgagaatgc gagagataca tcaaaagctt 1800
atcagaaaagt tcaatgctcg aggtcaaaaa tataccgtta atgccataca agaaacatgg 1860
aagaagaaaag accgtagccg ggtatcagat cggcatcatt ccgatgctgg tagaagtact 1920
cttggccgta ttctttgctt tggagccagt tcgggaaccc gccgagcgct tggtgacttg 1980
atcgctgggc tcccttctag gtcgcggcgt ttttattttt gaactcgacc ctgtagcggt 2040
cttgcggtgg aagcgcttct tggacgaagt ctttcttttc ttggaacggc tagtctcggt 2100
gtcttcatac tcttcggatg a 2121

```

<210> 188

<211> 1143

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267
Genomic sequence containing the coding region

<400> 188

```

atggacatct cgcaagaaac cgttgataaa atacgacgtt tcgcgcaaaa gcgccccaaaa 60
gcgaggaggt tctacgagga aactcggta aatccagcta attttgacgc ttacaatcgc 120
aagttggatg agacgttggc agagctgcag gctcaagtca aacgtcatga ggatgagctc 180
cgcaaggtac gtcaacaagt tgcctagaat ataagccgac tgtcacaaga gatttcatgc 240
atgaattagg aatactgaca agaggaacag ctacgcatga ccaccacgat cgagttcgct 300
caaattgggg cagatccttg ggcccgcac tcagaagtgc gcagagccaa gaaagcgat 360
gattctcttc tgcaatcggg aacgcgactg ccgagtcag gctcgccctt gccttcatta 420
cttgcggttg acgaggcgct tcgtctcgct aaggagagca agacctcaat ctactgacg 480
gcgagaaaaa tgtctgcgga tcgtcagcgc ttgaaagcgg aagaagccaa tttgcgcgat 540
gcgcaactga tcaaagacgg gttggagaaa aggattgagc ggctgaacgc agaaaaatcg 600
agtcaagtcc agaaaactcc tgcgcagctt gcgtatgatc tcgtcaagga gcagcaggaa 660
aagatcgaga gacttgatac taccacagaa gagctaaagt cctctctcta taaatttgct 720
gaagacacac ttgcccacat gcttgctgca gaaaatctgg gcggtccac tgctcgagat 780
gcgttggaat tttcgacac taccttaaaa gcgggctaca ctagccatgg gaagcctaag 840
aaacaaaaaa ctccggccgt ggggacttct gacagtggcc aacagcggat tgacgagctt 900
gttcgtcgcc aaactgcgca ggagggaac gacgaggcaa cccttttgaa caaaagagag 960
gcgccgcgcg ctgaaatgct agctcttctt actgctctgt tagatgcgga ttactcctat 1020
gtcgaccttc cgcacgagtc agcggcctcg cgctttctag taagagcgaa ggtagctcaa 1080
ttccatccgc gcgatgccag gaagcttcgg ttaattgatt ttgggcgctc attagtcgat 1140
tga 1143

```

<210> 189

<211> 1035

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267
Coding region without introns

<400> 189

```

atggacatct cgcaagaaac cgttgataaa atacgacgtt tcgcgcaaaa gcgccccaaaa 60
gcgaggaggt tctacgagga aactcggta aatccagcta attttgacgc ttacaatcgc 120
aagttggatg agacgttggc agagctgcag gctcaagtca aacgtcatga ggatgagctc 180
cgcaagttcg ctcaaatttg ggcagatcct tgggcccgcg tctcagaagt gcgcagagcc 240
aagaagcgt atgattctct tctgcaatcg gaaacgcgac tgccgagtc aggtcgccc 300
ttgccttcat tacttgcggt tgacgaggcg tctcgtctcg tcaaggagag caagacctca 360
atctcactga cggcgagaa actgtctgct gatcgtcagc gcttgaaagc ggaagaagcc 420
aatttgcgcg atgcgcaact gatcaaagac ggggttgaga aaaggattga gcggctgaac 480
gcagaaaaat cgagtcaagt ccagaaaact cctgcgcagc ttgcgtatga tctcgtcaag 540
gagcagcagg aaaagatcga gagacttgat actaccacag aagagctaaa gtcctctctc 600

```



```

tataaatttg tcgaagacac acttgcccca atgcttgctg cagaaaatct gggcgggtccc 660
actgtcggag atgcgttgga aatttcggac actaccttaa aagcgggcta cactagccat 720
gggaagccta agaaacaaaa aactccggcc gtgggggactt ctgacagtgg ccaacagcgg 780
attgacgagc ttgttcgtcg ccaaactgcg caggagggca acgagcaggc aacccttttg 840
aacaaaagag aggcggccgc cgctgaaatg cgagctcttc ttactgctct gttagatgcg 900
gattactcct atgtcgacct tccgcacgag tcagcggcct cgcgctttct agtaagagcg 960
aaggtagctc aattccatcc ggcgcgatgcc aggaagcttc ggttaattga ttttgggcgc 1020
tcattagtcg attga 1035

```

<210> 190

<211> 344

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267
Protein sequence

<400> 190

```

Met Asp Ile Ser Gln Glu Thr Val Asp Lys Ile Arg Arg Phe Ala Gln
1          5          10          15

Lys Arg Gln Lys Ala Glu Glu Phe Tyr Glu Glu His Ser Val Asn Pro
20        25        30

Ala Asn Phe Asp Ala Tyr Asn Arg Lys Leu Asp Glu Thr Leu Ala Glu
35        40        45

Leu Gln Ala Gln Val Lys Arg His Glu Asp Glu Leu Arg Lys Phe Ala
50        55        60

Gln Ile Gly Ala Asp Pro Trp Ala Arg Ile Ser Glu Val Arg Arg Ala
65        70        75        80

Lys Lys Ala Tyr Asp Ser Leu Leu Gln Ser Glu Thr Arg Leu Pro Ser
85        90        95

Pro Gly Ser Pro Leu Pro Ser Leu Leu Ala Val Asp Glu Ala Ser Arg
100       105       110

Leu Val Lys Glu Ser Lys Thr Ser Ile Ser Leu Thr Ala Glu Lys Leu
115       120       125

Ser Ala Asp Arg Gln Arg Leu Lys Ala Glu Glu Ala Asn Leu Arg Asp
130       135       140

Ala Gln Leu Ile Lys Asp Gly Leu Glu Lys Arg Ile Glu Arg Leu Asn
145       150       155       160

Ala Glu Lys Ser Ser Gln Val Gln Lys Thr Pro Ala Gln Leu Ala Tyr
165       170       175

Asp Leu Val Lys Glu Gln Gln Glu Lys Ile Glu Arg Leu Asp Thr Thr
180       185       190

Thr Glu Glu Leu Lys Ser Ser Leu Tyr Lys Phe Val Glu Asp Thr Leu
195       200       205

Ala Pro Met Leu Ala Ala Glu Asn Leu Gly Gly Pro Thr Val Gly Asp
210       215       220

```

Ala Leu Glu Ile Ser Asp Thr Thr Leu Lys Ala Gly Tyr Thr Ser His
 225 230 235 240

Gly Lys Pro Lys Lys Pro Lys Thr Pro Ala Val Gly Thr Ser Asp Ser
 245 250 255

Gly Gln Gln Arg Ile Asp Glu Leu Val Arg Arg Gln Thr Ala Gln Glu
 260 265 270

Gly Asn Glu Gln Ala Thr Leu Leu Asn Lys Arg Glu Ala Ala Ala Ala
 275 280 285

Glu Met Arg Ala Leu Leu Thr Ala Leu Leu Asp Ala Asp Tyr Ser Tyr
 290 295 300

Val Asp Leu Pro His Glu Ser Ala Ala Ser Arg Phe Leu Val Arg Ala
 305 310 315 320

Lys Val Ala Gln Phe His Pro Arg Asp Ala Arg Lys Leu Arg Leu Ile
 325 330 335

Asp Phe Gly Arg Ser Leu Val Asp
 340

<210> 191

<211> 2000

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA283; clone 11-6-20; contig 4910 region 9638-11637
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 191

tgaacctatg	taccatccac	tcctgagtc	tgctcagggg	aaatgcatgt	gagcaggtgc	60
cttctcacct	ctgctccttt	aatacttcat	tgcggggata	ttattccgtg	ctggacagct	120
tctgcaagat	cagtaattat	gtaggaacac	gaaaacaatg	ttctacacat	tagttttctc	180
ctgatgacca	tcttctcttt	gatcaatgca	gcagacaaca	aatcctgtcc	aatcatccca	240
acatactgtt	tcctaccttg	attggcgcaa	atccggcgac	aataatcaag	ggtagagtga	300
tggactaggc	tcaggcggtt	tgactttgca	aatccaattg	aattctgatc	agtgctaagc	360
cgatgatggc	gttgagcgac	caaggacaat	ttccgactga	gtcagcattt	tccctcgctc	420
gcgactcgcg	aggcgcggtc	caggacggga	ggtcttgga	aggctgaacg	gtcaatcaat	480
catcaaattg	gtaggatggt	gcgtaaatag	cccacatgcg	cataaaaagt	gatgagtgcc	540
gcacgggtat	cttcggttctt	gtttcctttt	ccgtctcacc	ccaagatcat	gggtcatgaa	600
ttgataatag	tatcgtcaac	tggcttagcg	tgatgactac	gtatcttttt	gagcgtcaag	660
ttcggctcgtt	tcaatcggag	tggttttctc	cgccaacgcc	tagtccattg	ctcccaagag	720
aggggctgat	aaatgacggc	gctcaggggc	ccaggggctt	catgtaggca	caatggaagt	780
aaaacgtatg	tacgaagaat	ggatcatctc	tcaaagtact	atactccgta	ctcttgcttg	840
tattctgata	tttcagttca	ataatcgaaa	aatagtgcg	cgcggtatgg	tcagatctt	900
atgcagatag	gacagtcagc	ccgccagtat	tacggagaac	ctaaggtact	catagtaaag	960
tatgatgata	cggccgcata	cgacctctaa	ttcatcgaat	actccagaag	cggctagcca	1020
ctttcctgaa	atcgaggtct	atccatggac	tcagcatctt	gtacggagta	caaactcctg	1080
ccagcttatt	ccaactgatg	accctggccc	ttatatgagc	aagcaggata	tgattgggag	1140
acttgagttg	tgtttggaac	cagctggtca	gccacggaat	gatattagga	ttactaaggt	1200
agctattgtc	tcacacaggt	atgcactgcg	gaacatggat	taattgatac	ttatgaaccc	1260
taactgcttt	ggaggggagg	tgatactcta	cctgagggaa	aggcgaacaa	ttacagagta	1320
atgataatgc	ataaataata	tctcatgatg	ttaccctgcc	tcgtcaaaca	tgaggtctcg	1380
ctttcgattg	tgaatccact	tctccatttt	tacgtcagac	taattccatt	taatcaatac	1440
ctctcgtatg	gggtaaatca	atgcaccgga	aatttacata	tgatatcaaa	agtagtagtt	1500
ctccgactag	ggaggatgga	gcaaggtaat	ctatatattat	tggtgctcg	tttgcaggcc	1560

aaacccaaaac	caacatgctc	tgtatcttag	cctccgtatc	tgatctcata	tctttgagga	1620
cattgattgg	attgtcgatc	ccaatgacgg	cgtgctgaga	ctgttctaaa	gagagctcaa	1680
aagaaataga	gcaaaaagtaa	gatcatctac	ggactatcta	cgctctatag	gagtttcaact	1740
ctgtgataat	ggctcacgcc	cacataaact	gtccatgacg	aaatcgatac	agcctcaaga	1800
aagccaacaa	tttttagtttg	gaagtcgaat	cacaccacat	aggttaacca	gcaaaagcgc	1860
agacctccaa	taaaggttcg	ctcatcggtc	ccttctgctg	ctactttgga	gctaaagctg	1920
cgcgtctgta	catcttgacc	tccttcggcc	tctcctttgc	gctgtgctca	gttttccctt	1980
cttttgtctc	ttggaactga					2000

<210> 192

<211> 4336

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899
region 472441-476776

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 192

acgattggcc	aatcgtttgc	tgtaatgctt	ggcggcttct	tggcattgcc	cagcccaagg	60
tgctcacgtg	ggtgggatga	tgggcatgtc	gactgtcgtg	tgcgctcatcg	ggctgggagg	120
cggcaaatgc	tcgcgcacccg	accacaggaa	ttcggccaag	attctggatc	gattgcccct	180
tatgtatgcg	aaggtttggg	gatgtgattg	gtgtgcagcg	taaacgagta	cggattgata	240
agagtgccaa	gatttgaacc	actgttcacg	tcattggagg	gggtttccgg	cacgccgggt	300
aggagtgaga	cagagtgtac	taaatatgtc	gcgatacccc	cgcaacgacg	ggagaagaaa	360
atctgggttct	acaacctagg	ctttaatttc	caagttgatt	tcaagtcgtt	gtgtatggac	420
tctcactcgc	ttgaagatac	gatatacatg	aagcctcctt	aggataactg	caactggaata	480
gaacattttc	gttatataac	atgggtgcgc	agaagaagca	atcctctgat	aactctcagg	540
ctttgtctca	gcctgctcat	gcgcttcgct	atgaggatgt	ccttcgtgag	ctggccgctg	600
atccagacca	gggtctgacc	gtgggggagg	cgaagcgaag	actccaacaa	tatgggtccga	660
atgaactgga	aggggggagag	ggtgtttcca	ttgtcaagat	tgctattagg	cagatcgcaa	720
atgccatgat	gctgggttagt	ctctcccttt	tggttagacag	acaactgacg	acaactgacg	780
acagcaggtc	ctgatcatcg	ccatggcggt	cagtttcggc	attcaatcct	ggattgaggg	840
tggtgtcatt	ggggctgtca	ttggctctaa	cattgtggta	ggtgtctatc	aagactatgc	900
cgcagagaaa	acgatggatt	cccttcgata	ggttagttct	cccaccggaa	ctgtcacgcg	960
tgatggcaaa	accagtacca	ttcctgcca	cgagattgtc	cccggggaca	tgattgaact	1020
caaagtggga	gacacgggtc	ctgcggatct	tcggtgcgta	aagagttacc	agaaaatatc	1080
gttcccgttc	actaaccgcc	gataggctcg	ttgatgcaat	gaatttcgaa	accgacgagg	1140
ccctcctgac	tgccgagtcg	ctgccgggtg	agaaagaggt	cgataccact	tttgacccag	1200
acacgggacc	tggtgatcgg	ttgaatatgt	cgtatagttc	ctccacgggtg	acgagaggcc	1260
gcgctcgggg	cgttggtatc	agcacgggga	tgcaaaccca	gattggagcc	atcgccgctg	1320
ctctccgcgc	cagcgactcc	aagaggcggc	ccgtcaagcg	cgggtcccga	ggagaaacca	1380
agaagcgatg	gtacgtgcag	gcgtggaccc	tgacttgacg	ggatgccgtg	ggacggttcc	1440
tggaatcaa	cgttggcaca	ccgctgcagc	gcaaactctc	gaaactggct	ttggcccttt	1500
tcgccattgc	catcatcttc	gccatcattg	tcattggcgt	caatgggttc	cgcaatgaca	1560
aggaggtcat	catctacgca	gtcgcaacag	gtcttgcaat	gatcccggcc	tgccctggtg	1620
tggtcctgac	cattaccatg	gcggttgga	ccaagcaa	ggttgaaaga	catgtcattg	1680
tccggaagct	tgattccctt	gaagccctgg	gcgctgtgac	taacattttg	tcagacaaaa	1740
cgggaaccct	cacccagggg	cgcatggtcg	ccaaacgggc	gtggattccc	tctgttgga	1800
ccttctcggg	gggtctcttc	aataaccctt	tgaacccgga	agagggcgac	cttagcctgc	1860
tgctgaccc	gccgctcaaa	gttgccctg	acgctcatgg	agagccttcc	cggccggagg	1920
atctgctcaa	ggacaatcct	cttttgagc	aatatctgaa	cgtggccgcc	atggcaaacc	1980
ttgcccattg	gcacaggtcc	gagcacaatg	aatggcaggc	tcgtggtgaa	ccgaccgaca	2040
ttgcgattca	ggtgtttgcc	tcgcgcttta	actggggacg	cgatcgctgg	accaaaggcg	2100
agaagcctgt	ttggcgccaa	aaagctgaat	atccatttga	ttctactgtg	aaaaagatgt	2160
ctgtcatctt	taagaacacc	aatgatgatc	gggagatgat	cttcaccaag	ggcgcgggtg	2220
aacgtgtcat	cgaggcttgc	accaccgta	cctggacagc	tggttccgac	ccgatcgcc	2280
tggacgagaa	cataaaggag	gaaatcttgc	agaacatgga	agctctcgca	aaggaggcc	2340
tgcgagttct	ctgcctcgcc	tgctcgggaga	atcacaaccc	cgtcaaaggg	gaagttgtcc	2400

ctgcgcgtga	ggaagtggag	aaagatctca	ctttctgtgg	actcatcggg	ctgtatgacc	2460
ctccccgacc	tgagacggcc	ggcgctattg	acgagtgcta	cgcgcgtggg	atttcggttc	2520
acatggtcac	ggcgaccac	cgggtactg	cgcgagcgat	tgcagcgag	gttggcatca	2580
ttccagccaa	catggacagt	cttgccaaag	atgttgcgga	cgccatggtg	atgactgcca	2640
gtcagtttga	taagttgaca	gacgaggaaa	tcgatgcgtt	gcctactctg	cctgctgtga	2700
ttgctcggtg	cgtcccaac	acaaagggtt	ggatgattga	tgcccttcat	cgtcggggtc	2760
ggtttgcggc	aatgactggt	gatggagtca	atgactcgcc	atcgttgaag	cgggcagatg	2820
ttggaattgc	tatgggacaa	tcgggggtccg	atgtggccaa	agacgcttcg	gaactggtgt	2880
tgaactgatga	caactttgcg	tcgattatca	acggaattga	ggaggggtcgt	cgtatttttg	2940
ataatattca	gaaattcgtc	ctgcatcttc	tggcggaata	cgtcgggtctc	gccctcacgc	3000
ttctgatagg	tctgtgtttc	aaagatgaca	acgggcaatc	tgtgtttcct	attgctcctg	3060
tcgaaattct	atggatcatc	atgatcacct	cggggtccc	ggacatggga	ctgggtatgg	3120
agatcgcggc	tccggatatc	atggaccgtc	ctcctcaaag	cgtaagtaca	tcagtcactc	3180
tttctgggat	catatactaa	cgacaacaga	aacaagggtat	tttcacctgg	gaagtcatag	3240
tcgacacccat	ggtctacggc	gtctggatgg	cggctctctg	tctcgctctc	ttctcgctcg	3300
tcctcttttg	ttggggagat	ggcaacctgg	cctcgggctg	caacagcgac	tacagccccg	3360
aatgcgacgg	tgtgttcgcg	gcccagacta	cgaccttcgt	gtgcatgaca	tggttcgctc	3420
tcttctctcg	ctgggagatg	attgatatgc	gccgcagctt	cttccgcatg	cagcccaatt	3480
ccaagcgcta	tttcacccag	tggatgtttg	acgtctggcg	caacaagtgt	ctgttcagcg	3540
gcatcatgat	tggattcgtc	acgaccttcc	ccatcctgta	catccctgtg	atcaatgacg	3600
ttgtcttcaa	gcatgtcggg	atctcctggg	agtgggggtg	ggtgtttgtc	gaagcgattc	3660
ttttcttctg	tggctgcgag	gcctggaagt	ggtgcaagcg	catttatttc	aggcacacca	3720
gccaaaagga	aactggcaga	gaaaggggtac	ttcgggactt	tagccgttat	accaccatga	3780
gcaggtccga	gacccaagca	acgggtgacc	tcaacgtgga	aaagtcgatg	gtttagatct	3840
ggcaatagga	caggatagca	gcagatggag	ggcaggggag	cgactgcgtg	tatttgcatg	3900
catctaattg	gtggccactg	gttttcatta	agcagaatgt	acatagatat	gaatagaagt	3960
agcgatttat	cttttttttc	cgcctttcgg	tttccccccc	ttctgcaggt	tcacgagtaa	4020
ttgactttat	cctcactcta	gagtcctagt	gatatggtat	gtctttgtaa	atatgcaatc	4080
agtctcagtt	tatcatattc	attctgattc	actataactg	gattatataa	ttctgtatgc	4140
atacttatcg	ccttatctaa	aaaggcagta	atttggcaca	tccacacggg	tccttgatat	4200
atactctcgt	ccatgggtac	atcataggct	tcataccctt	gatatatatc	gggaaccctt	4260
cagcacaaca	gacaagtcaa	caacaaaactg	atgaaaatag	attagatagt	attacagtac	4320
tacctatgta	gttcta					4336

<210> 193

<211> 3336

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899
region 472441-476776

Genomic sequence containing the coding region

<400> 193

atgggtgcgc	agaagaagca	atcctctgat	aactctcagg	ctttgtctca	gcctgctcat	60
gcgcttcgct	atgaggatgt	ccttcgtgag	ctggccgctg	atccagacca	gggtctgacc	120
gtgggggagg	cgaagcgaag	actccaacaa	tatggtccga	atgaactgga	agggggagag	180
ggtgtttcca	ttgtcaagat	tgtcattagg	cagatcgcaa	atgccatgat	gctgggttagt	240
ctctcccttt	tgttagacag	acaacgacag	acaactgacg	acagcaggtc	ctgatcatcg	300
ccatggcggt	cagtttcggc	attcaatcct	ggattgaggg	tgggtgcatt	ggggctgtca	360
ttggtctaaa	cattgtggta	ggtgtctatc	aagactatgc	cgcagagaaa	acgatggatt	420
cccttcgata	gttgagttct	cccaccggaa	ctgtcacgcg	tgatggcaaa	accagtacca	480
ttcctgccaa	cgagattgtc	cccggggaca	tgattgaact	caaagttgga	gacacggttc	540
ctgcggatct	tcggtgcgta	aagagttacc	agaaaatatc	gttcccgttc	actaaccgcc	600
gataggctcg	ttgatgcaat	gaatttcgaa	accgacgagg	ccctcctgac	tggcagatcg	660
ctgccgggtgc	agaaaagagg	cgataccact	tttgacccag	acacgggacc	tgggtgatcgg	720
ttgaatattg	cgtatagttc	ctccacgggtg	acgagaggcc	gcgctcgggg	cgttggtatc	780
agcacgggga	tgcaaaccga	gatttgagcc	atcgccgctg	ctctccgcgc	cagcgactcc	840
aagaggcggc	ccgtcaagcg	cgggtcccag	ggagaaacca	agaagcgatg	gtacgtgcag	900

gcgtggaccc	tgacttgac	ggatgccgtg	ggacggttcc	tggaatcaa	cgttggcaca	960
ccgtgacgc	gcaaaactctc	gaaactggct	ttggcccttt	tcgccattgc	catcatcttc	1020
gccatcattg	tcatgggcgt	caatgggttc	cgcaatgaca	aggagggtcat	catctacgca	1080
gtcgcaacag	gtcttgcaat	gatcccgcc	tgccctggtg	tggtcctgac	cattaccatg	1140
gcggttgaa	ccaagcaaat	ggttgaaaga	catgtcattg	tccggaagct	tgattccctt	1200
gaagccctgg	gcgctgtgac	taacatttgc	tcagacaaaa	cggaaccct	caccagggg	1260
cgcatggctg	ccaaacgggc	gtggattccc	tctgttgga	ccttctcggt	gggtcttct	1320
aataaccctt	tgaaccggga	agagggcgac	cttagcctgc	tgcccgacc	gccggtcaaa	1380
gttggccctg	acgctcatgg	agagccttcc	cgcccgagg	atctgctcaa	ggacaatcct	1440
cttttgagc	aatatctgaa	cgtggccgcc	atggcaaac	ttgcccatgt	gcacagggtcc	1500
gagcacaatg	aatggcaggc	tcgtggtgaa	ccgaccgaca	ttgcgattca	ggtgtttgcc	1560
tcgcgcttta	actggggacg	cgatcgctgg	accaaaggcg	agaagcctgt	ttggcgccaa	1620
aaagctgaat	atccatttga	ttctactgtg	aaaaagatgt	ctgtcatctt	taagaacacc	1680
aatgatgatc	gggagatgat	cttcaccaag	ggcgcggtgg	aacgtgtcat	cgaggcttgc	1740
accaccgtca	cctggacagc	tggttccgac	ccgatcgcc	tgacgagaa	cataaaggag	1800
gaaatcttgc	agaacatgga	agctctcgca	aaggagggcc	tgcgagttct	ctgcctcgcc	1860
tgtcgggaga	atcacaaccc	cgtcaaagg	gaagtgtcc	ctgcgctga	ggaagtggag	1920
aaagatctca	ctttctgtgg	actcatcggt	ctgtatgacc	ctccccgacc	tgagacggcc	1980
ggcgctattg	acgagtgtca	ccgcgctggg	atttcggttc	acatggtcac	gggcgaccac	2040
ccgggtactg	cgcgagcgat	tgacgcgag	gttggcatca	ttccagccaa	catggacagt	2100
cttgccaaag	atgttgcgga	cgccatgggtg	atgactgcca	gtcagtttga	taagttgaca	2160
gacgaggaaa	tcgatgcgtt	gcctactctg	cctgctgtga	ttgctcggtg	cgctcccaac	2220
acaaagggttc	ggatgattga	tgcccttcat	cgctcggttc	ggtttgcggc	aatgactggt	2280
gatggagtca	atgactcgcc	atcgttgaag	cgggcagatg	ttggaattgc	tatgggacaa	2340
tcgggggtccg	atgtggccaa	agacgcttcg	gaactggtgt	tgactgatga	caactttgcg	2400
tcgattatca	acggaattga	ggagggtcgt	cgtatttttg	ataatattca	gaaattcgtc	2460
ctgcactcttc	tggcggaaaa	cgctcggtctc	gccctcacgc	ttctgatagg	tctgtgtttc	2520
aaagatgaca	acgggcaatc	tgtgtttcct	attgtcctctg	tcgaaattct	atggatcatc	2580
atgatcacct	ccgggctccc	ggacatggga	ctgggtatgg	agatcgcggc	tccggatatac	2640
atggaccgtc	ctcctcaaag	cgtaagtaca	tcagtcactc	tttctgggat	catatactaa	2700
cgacaacaga	aacaaggat	tttcacctgg	gaagtcatag	tcgacaccat	ggtctacggc	2760
gtctggatgg	cggtctctctg	tctcgctctc	ttctcgctcg	tcctcttttg	ttggggagat	2820
ggcaacctgg	cctcggtctg	caacagcgac	tacagccccg	aatgagcgg	tgtgttccgc	2880
gcccagacta	cgacctctgt	gtgcatgaca	tggttcgctc	tcttctcgc	ctgggagatg	2940
attgatatgc	gcccagctt	cttcgcatg	cagcccaatt	ccaagcgcta	tttcacccag	3000
tggatgtttg	acgtctggcg	caacaagttt	ctgttcagcg	gcatcatgat	tggattcgtc	3060
acgaccttcc	ccatcctgta	catccctgtg	atcaatgacg	ttgtcttcaa	gcatgtcggt	3120
atctcctggg	agtgggtgt	ggtgtttgtc	gaagcgattc	ttttcttcgc	tggctgcgag	3180
gcctggaagt	ggtgcaagcg	catttatttc	aggcacacca	gccaaaagga	aactggcaga	3240
gaaagggtac	ttcgggactt	tagccgttat	accaccatga	gcagggtccga	gacccaagca	3300
acgggtgacc	tcaacgtgga	aaagtcgatg	gtttag			3336

<210> 194

<211> 3180

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899
region 472441-476776

Coding region without introns

<400> 194

atgggtgcgc	agaagaagca	atcctctgat	aactctcagg	ctttgtctca	gcctgctcat	60
gcgcttcgct	atgaggatgt	ccttcgtgag	ctggccgtcg	atccagacca	gggtctgacc	120
gtgggggagg	cgaagcgaag	actccaacaa	tatgggtccga	atgaactgga	agggggagag	180
ggtgtttcca	ttgtcaagat	tgtcattagg	cagatcgcaa	atgccatgat	gctggtcctg	240
atcatcgcca	tggcggtcag	tttcggcatt	caatcctgga	ttgagggtgg	tgtcattggg	300
gctgtcattg	gtctaaacat	tgtggttaggt	gtctatcaag	actatgccgc	agagaaaacg	360
atggattccc	ttcgatcggt	gagttctccc	accggaactg	tcacgcgtga	tggcaaaacc	420

```

agtagcattc ctgccaaacga gattgtcccc ggggacatga ttgaactcaa agttggagac 480
acggttcctg cggatcttcg gctcgttgat gcaatgaatt tcgaaaaccga cgaggccctc 540
ctgactggcg agtcgctgcc ggtgcagaaa gaggtcgata ccacttttga cccagacacg 600
ggacctggtg atcggttgaa tattgcgtat agttcctcca cggtgacgag aggccgcgct 660
cggggcggtt ttatcagcac ggggatgcaa accgagattg gagccatcgc cgctgctctc 720
cgcgccagcg actccaagag gcggcccgtc aagcgcggtc ccgagggaga aaccaagaag 780
cgatggtacg tgcaggcggtg gaccctgact tgcacggatg ccgtgggacg gttcctggga 840
atcaacggtt gcacaccgct gcagcgcaaa ctctcgaaac tggctttggc ctttttcgcc 900
attgccatca tcttcgccat cattgtcatg ggcgtcaatg ggttccgcaa tgacaaggag 960
gtcatcatct acgcagtcgc aacaggctctt gcaatgatcc cggcctgcct ggtggtggtc 1020
ctgaccatta ccatggcggt tggaaaccaag caaatggttg aaagacatgt cattgtccgg 1080
aagcttgatt cccttgaagc cctgggcgct gtgactaaca tttgctcaga caaaacggga 1140
accctcaccg aggggcgcgt ggtcgccaaa cgggcgtgga ttccctctgt tggcaccttc 1200
tcggtggggt cttctaataa ccccttgaac ccggaagagg gcgaccttag cctgctgcct 1260
gaccgcggcg tcaaagttgg ccctgacgct catggagagc ctccccggcc ggaggatctg 1320
ctcaaggaca atcctctttt ggagcaatat ctgaacgtgg ccgccatggc aaaccttgcc 1380
catgtgcaca ggtccgagca caatgaatgg caggctcgtg gtgaaccgac cgacattgag 1440
attcaggtgt ttgcctcgcg ctttaactgg ggacgcgac gctggacca aaggcagaag 1500
cctgtttggc gccaaaaaagc tgaatatcca tttgattcta ctgtgaaaaa gatgtctgtc 1560
atctttaaga acaccaatga tgatcgggag atgatcttca ccaagggcgc ggtggaacgt 1620
gtcatcgagg cttgcaccac cgtcacctgg acagctggtt ccgacccgat cgccttgagc 1680
gagaacataa aggaggaaat cttgcagaa atggaagctc tcgcaaagga gggcctgcga 1740
gttctctgcc tcgcctgtcg ggagaatcac aaccccgcta aaggggaagt tgtccctgag 1800
cgtgaggaag tggagaaaga tctcactttc tgtggactca tcggtctgta tgacctccc 1860
cgacctgaga cggccggcgc tattgacgag tgctaccgag ctgggatttc ggttcacatg 1920
gtcacgggag accaccggg tactgcgcga gcgattgcag cgcaggttgg catcattcca 1980
gccaacatgg acagtcttgc caaagatggt gcggacgcca tggatgac tgccagtcag 2040
tttgataagt tgacagcga ggaaatcgat cggttgccta ctctgcctgc tgtgattgct 2100
cgggtcgctc ccaacacaaa gggttcggatg attgatgccc ttcatcgctc gggtcggttt 2160
gcggaatga ctggtgatgg agtcaatgac tcgccatcgt tgaagcgggc agatgttgga 2220
attgctatgg gacaatcggg gtccgatgtg gccaaagacg cttcggaact ggtgttgact 2280
gatgacaact ttgcgtcgat tatcaacgga attgaggagg gtcgtcgat ttttgataat 2340
attcagaaat tcgtcctgca tcttctggcg gaaaacgtcg gtctcgccct cactctctg 2400
ataggtctgt gtttcaaaga tgacaacggg caatctgtgt ttctatttgc tctgtcgaa 2460
attctatgga tcatcatgat cacctccggg ctcccggaca tgggactggg tatggagatc 2520
gcggtcccg atatcatgga ccgtcctcct caaagcgtaa gtattttcac ctgggaagtc 2580
atagtcgaca ccatgggtcta cggcgtctgg atggcggtc tctgtctcgc ctctttctcg 2640
ctcgtcctct ttggttgggg agatggcaac ctggcctcgg gctgcaacag cgactacagc 2700
cccgaatgag acggtgtgtt ccgcgcccga gctacgacct tcgtgtgcat gacatgggtc 2760
gctctcttcc tcgcctggga gatgattgat atgcgcgca gcttcttccg catgcagccc 2820
aattccaagc gctatttcac ccagtggatg tttgacgtct ggcgcaacaa gtttctgttc 2880
agcggcatca tgattggatt cgtcacgacc ttccccatcc tgtacatccc tgtgatcaat 2940
gacgttgtct tcaagcatgt cggatatctc tgggagtggg gtgtggtgtt tgtcgaagcg 3000
attcttttct tcgctggctg cgaggcctgg aagtgggtgca agcgattta tttcaggcac 3060
accagccaaa aggaaactgg cagagaaagg gtacttcggg actttagccg ttataccacc 3120
atgagcaggt ccgagaccca agcaacgggt gacctcaacg tggaaaagtc gatggtttag 3180

```

<210> 195

<211> 1059

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899
region 472441-476776
Protein sequence

<400> 195

```

Met Gly Ala Gln Lys Lys Gln Ser Ser Asp Asn Ser Gln Ala Leu Ser
1              5              10              15

```

Gln Pro Ala His Ala Leu Arg Tyr Glu Asp Val Leu Arg Glu Leu Ala
 20 25 30
 Val Asp Pro Asp Gln Gly Leu Thr Val Gly Glu Ala Lys Arg Arg Leu
 35 40 45
 Gln Gln Tyr Gly Pro Asn Glu Leu Glu Gly Gly Glu Gly Val Ser Ile
 50 55 60
 Val Lys Ile Val Ile Arg Gln Ile Ala Asn Ala Met Met Leu Val Leu
 65 70 75 80
 Ile Ile Ala Met Ala Val Ser Phe Gly Ile Gln Ser Trp Ile Glu Gly
 85 90 95
 Gly Val Ile Gly Ala Val Ile Gly Leu Asn Ile Val Val Gly Val Tyr
 100 105 110
 Gln Asp Tyr Ala Ala Glu Lys Thr Met Asp Ser Leu Arg Ser Leu Ser
 115 120 125
 Ser Pro Thr Gly Thr Val Thr Arg Asp Gly Lys Thr Ser Thr Ile Pro
 130 135 140
 Ala Asn Glu Ile Val Pro Gly Asp Met Ile Glu Leu Lys Val Gly Asp
 145 150 155 160
 Thr Val Pro Ala Asp Leu Arg Leu Val Asp Ala Met Asn Phe Glu Thr
 165 170 175
 Asp Glu Ala Leu Leu Thr Gly Glu Ser Leu Pro Val Gln Lys Glu Val
 180 185 190
 Asp Thr Thr Phe Asp Pro Asp Thr Gly Pro Gly Asp Arg Leu Asn Ile
 195 200 205
 Ala Tyr Ser Ser Ser Thr Val Thr Arg Gly Arg Ala Arg Gly Val Val
 210 215 220
 Ile Ser Thr Gly Met Gln Thr Glu Ile Gly Ala Ile Ala Ala Ala Leu
 225 230 235 240
 Arg Ala Ser Asp Ser Lys Arg Arg Pro Val Lys Arg Gly Pro Glu Gly
 245 250 255
 Glu Thr Lys Lys Arg Trp Tyr Val Gln Ala Trp Thr Leu Thr Cys Thr
 260 265 270
 Asp Ala Val Gly Arg Phe Leu Gly Ile Asn Val Gly Thr Pro Leu Gln
 275 280 285
 Arg Lys Leu Ser Lys Leu Ala Leu Ala Leu Phe Ala Ile Ala Ile Ile
 290 295 300
 Phe Ala Ile Ile Val Met Gly Val Asn Gly Phe Arg Asn Asp Lys Glu
 305 310 315 320
 Val Ile Ile Tyr Ala Val Ala Thr Gly Leu Ala Met Ile Pro Ala Cys
 325 330 335

Leu Val Val Val Leu Thr Ile Thr Met Ala Val Gly Thr Lys Gln Met
 340 345 350
 Val Glu Arg His Val Ile Val Arg Lys Leu Asp Ser Leu Glu Ala Leu
 355 360 365
 Gly Ala Val Thr Asn Ile Cys Ser Asp Lys Thr Gly Thr Leu Thr Gln
 370 375 380
 Gly Arg Met Val Ala Lys Arg Ala Trp Ile Pro Ser Val Gly Thr Phe
 385 390 395 400
 Ser Val Gly Ser Ser Asn Asn Pro Leu Asn Pro Glu Glu Gly Asp Leu
 405 410 415
 Ser Leu Leu Pro Asp Pro Pro Val Lys Val Gly Pro Asp Ala His Gly
 420 425 430
 Glu Pro Ser Arg Pro Glu Asp Leu Leu Lys Asp Asn Pro Leu Leu Glu
 435 440 445
 Gln Tyr Leu Asn Val Ala Ala Met Ala Asn Leu Ala His Val His Arg
 450 455 460
 Ser Glu His Asn Glu Trp Gln Ala Arg Gly Glu Pro Thr Asp Ile Ala
 465 470 475 480
 Ile Gln Val Phe Ala Ser Arg Phe Asn Trp Gly Arg Asp Arg Trp Thr
 485 490 495
 Lys Gly Glu Lys Pro Val Trp Arg Gln Lys Ala Glu Tyr Pro Phe Asp
 500 505 510
 Ser Thr Val Lys Lys Met Ser Val Ile Phe Lys Asn Thr Asn Asp Asp
 515 520 525
 Arg Glu Met Ile Phe Thr Lys Gly Ala Val Glu Arg Val Ile Glu Ala
 530 535 540
 Cys Thr Thr Val Thr Trp Thr Ala Gly Ser Asp Pro Ile Ala Leu Asp
 545 550 555 560
 Glu Asn Ile Lys Glu Glu Ile Leu Gln Asn Met Glu Ala Leu Ala Lys
 565 570 575
 Glu Gly Leu Arg Val Leu Cys Leu Ala Cys Arg Glu Asn His Asn Pro
 580 585 590
 Val Lys Gly Glu Val Val Pro Ala Arg Glu Glu Val Glu Lys Asp Leu
 595 600 605
 Thr Phe Cys Gly Leu Ile Gly Leu Tyr Asp Pro Pro Arg Pro Glu Thr
 610 615 620
 Ala Gly Ala Ile Asp Glu Cys Tyr Arg Ala Gly Ile Ser Val His Met
 625 630 635 640
 Val Thr Gly Asp His Pro Gly Thr Ala Arg Ala Ile Ala Ala Gln Val
 645 650 655
 Gly Ile Ile Pro Ala Asn Met Asp Ser Leu Ala Lys Asp Val Ala Asp

660					665					670					
Ala	Met	Val	Met	Thr	Ala	Ser	Gln	Phe	Asp	Lys	Leu	Thr	Asp	Glu	Glu
	675						680					685			
Ile	Asp	Ala	Leu	Pro	Thr	Leu	Pro	Ala	Val	Ile	Ala	Arg	Cys	Ala	Pro
	690					695					700				
Asn	Thr	Lys	Val	Arg	Met	Ile	Asp	Ala	Leu	His	Arg	Arg	Gly	Arg	Phe
	705					710					715				720
Ala	Ala	Met	Thr	Gly	Asp	Gly	Val	Asn	Asp	Ser	Pro	Ser	Leu	Lys	Arg
				725					730					735	
Ala	Asp	Val	Gly	Ile	Ala	Met	Gly	Gln	Ser	Gly	Ser	Asp	Val	Ala	Lys
			740					745					750		
Asp	Ala	Ser	Glu	Leu	Val	Leu	Thr	Asp	Asp	Asn	Phe	Ala	Ser	Ile	Ile
			755				760					765			
Asn	Gly	Ile	Glu	Glu	Gly	Arg	Arg	Ile	Phe	Asp	Asn	Ile	Gln	Lys	Phe
	770					775					780				
Val	Leu	His	Leu	Leu	Ala	Glu	Asn	Val	Gly	Leu	Ala	Leu	Thr	Leu	Leu
	785					790					795				800
Ile	Gly	Leu	Cys	Phe	Lys	Asp	Asp	Asn	Gly	Gln	Ser	Val	Phe	Pro	Ile
				805					810					815	
Ala	Pro	Val	Glu	Ile	Leu	Trp	Ile	Ile	Met	Ile	Thr	Ser	Gly	Leu	Pro
			820					825					830		
Asp	Met	Gly	Leu	Gly	Met	Glu	Ile	Ala	Ala	Pro	Asp	Ile	Met	Asp	Arg
		835					840					845			
Pro	Pro	Gln	Ser	Val	Ser	Ile	Phe	Thr	Trp	Glu	Val	Ile	Val	Asp	Thr
	850					855					860				
Met	Val	Tyr	Gly	Val	Trp	Met	Ala	Ala	Leu	Cys	Leu	Ala	Ser	Phe	Ser
	865					870					875				880
Leu	Val	Leu	Phe	Gly	Trp	Gly	Asp	Gly	Asn	Leu	Ala	Ser	Gly	Cys	Asn
				885					890					895	
Ser	Asp	Tyr	Ser	Pro	Glu	Cys	Asp	Gly	Val	Phe	Arg	Ala	Arg	Ala	Thr
			900					905					910		
Thr	Phe	Val	Cys	Met	Thr	Trp	Phe	Ala	Leu	Phe	Leu	Ala	Trp	Glu	Met
			915				920					925			
Ile	Asp	Met	Arg	Arg	Ser	Phe	Phe	Arg	Met	Gln	Pro	Asn	Ser	Lys	Arg
	930					935					940				
Tyr	Phe	Thr	Gln	Trp	Met	Phe	Asp	Val	Trp	Arg	Asn	Lys	Phe	Leu	Phe
	945					950					955				960
Ser	Gly	Ile	Met	Ile	Gly	Phe	Val	Thr	Thr	Phe	Pro	Ile	Leu	Tyr	Ile
				965					970					975	
Pro	Val	Ile	Asn	Asp	Val	Val	Phe	Lys	His	Val	Gly	Ile	Ser	Trp	Glu
			980					985					990		

Trp Gly Val Val Phe Val Glu Ala Ile Leu Phe Phe Ala Gly Cys Glu
 995 1000 1005

Ala Trp Lys Trp Cys Lys Arg Ile Tyr Phe Arg His Thr Ser Gln
 1010 1015 1020

Lys Glu Thr Gly Arg Glu Arg Val Leu Arg Asp Phe Ser Arg Tyr
 1025 1030 1035

Thr Thr Met Ser Arg Ser Glu Thr Gln Ala Thr Gly Asp Leu Asn
 1040 1045 1050

Val Glu Lys Ser Met Val
 1055

<210> 196

<211> 2059

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Homologue GmZnf1; Phylum CEA284.2;

contig 4899 region 477626-479684

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 196

cgccgaacta	tggggcatat	cggtagccaa	caccacttta	ctatactgtc	acgcgagtca	60
taaategcag	atggcccagt	tccagccctg	acaagagtgt	cacacttggt	ctattacgga	120
atgggcccgt	tcccgatgta	accgcacaag	ccgctatctt	ccctggaatg	ttggcacaag	180
gctacctatt	caggcgctca	agaatgccga	tgcctgaatt	cgcagttgac	tggcaagttt	240
catgagcgat	gtggcttcac	ttttggccag	aaacattggc	tgttccatct	cagcgagcag	300
ggtttcaaac	ttggatgcct	tggtgccttt	ccacatgagg	ttaagcacca	ttggctttgg	360
atattttgag	acgcatactg	tgctgtggca	cagtcagtgc	atttgtagcc	agtggctgtg	420
ttgtcatggt	cgtgaagggtg	gattagagtc	tggttggtgc	tgaagatgta	taggagaaaa	480
tagcatataa	ggggactgag	atgtctgtgg	ttgttcttgt	ttccaagcca	acagcacatt	540
tctcagaatt	ggcatctcat	cacagagtcc	gtgtaattat	cacattagca	aaagccacaa	600
tgtcccaccc	cgatctatcg	accattctcg	aggtctaccc	cgaatgcgaa	gtcacctgct	660
acgggtacgc	tcccagccaa	cggcgccgct	gcagaatgcg	aaccaggaaa	gacaaccgag	720
acagggcttc	gtaccttctc	gaagagggca	ccagatatct	tcagcgcggc	ctccccgtcg	780
acggtctgct	tattgagcta	gccccgctag	ttctctgcac	acgcttccac	caataccagg	840
cagacgactt	ggtccgggac	tggcggggcca	agctgcggga	gttccagcag	cagactcttc	900
tgaatgctat	gctgaaatcg	ctccaagagc	ttgtggacag	tcgggcgcgt	tcgcgtgctg	960
ctaggtcggc	gggtcggcgt	ctcccagaaa	gagtttctgag	tccgacacgg	ctggagaggt	1020
cgggtgctat	tgtaacagag	gaagaaccgg	ctgctcctga	aagagaggaa	gaggaggaag	1080
aaagaggaga	tagggaggac	gagcctgaac	cagaaccoga	acctgaacct	gaacttacct	1140
ccagccggtc	atctacggag	acttcctcgc	cagccgttga	ggctcatgtc	gcggagccaa	1200
ccgttcctca	gactgagtcc	agaagagtca	ctcgcaaac	aatcgaagga	gactgtacta	1260
tctgcctgtg	tcctctacga	gaacaagaca	gtgatgaaaa	cggcgaggga	tcagaagatc	1320
gcgatgatga	gaatgaggat	gatgcggcgg	gcacagggtc	cggcacagcg	tccgacgagc	1380
acgacgcccc	cgaagaacat	gacgatgacg	accttgata	ttgcaaaaac	cagtgcggta	1440
cgaactatca	caaagcctgt	attgacgtgt	ggcatgctac	tcagcgtaca	tttgaaactc	1500
cacgtgggga	tcctatcggc	ctgtcctgcc	cgtactgtcg	agcagcatgg	tcctcctgat	1560
ttcttcattc	tgcggggagt	ctcggcggtt	gttacttatt	tttgtatccc	aattccttct	1620
cacgttcttg	ttgcaatacg	tcagatatatt	ccttgtagag	ttatgcctgg	gggtgattat	1680
gagtacataa	cggccttggt	cagaattata	ttaatagcag	tttcctgggt	ctgcaaatat	1740
agtcgtgttg	gccttcaagc	ttgtagctga	gataaatgga	tacatagatg	gctctcttct	1800
atcgtgatga	tcattcccac	acgttggttc	tctcttcgcc	tgtgtctcga	tctcttgaat	1860
ctcgcctcga	cctcggctcc	agctagaagc	atcgaataca	atagctcctg	acaatggact	1920
gttctctgaa	ggatgagtgg	tctcaatgaa	tgtgaccgct	tgccgcgatt	ggcctcgaag	1980

acttaaagga gcaggcttct tttctgggca gagcggagtg aagcttctga accgcctcag 2040
gcaccgcgaa cctggagct 2059

<210> 197
<211> 1059
<212> DNA
<213> *Aspergillus fumigatus*

<220>
<223> Homologue GmZnf1; Phylum CEA284.2;
contig 4899 region 477626-479684
Genomic sequence containing the coding region

<400> 197
atgtctgtgg ttgttcttgt ttccaagcca acagcacatt tctcagaatt ggcatctcat 60
cacagagtcc gtgtaattat cacattagca aaagccacaa tgtcccaccc cgatctatcg 120
accattctcg aggtctaccc cgaatgcgaa gtcacctgct acgggtacgc tcccagccaa 180
cggcgccgct gcagaatgcg aaccaggaaa gacaaccgag acagggcttc gtaccttctc 240
gaagagggca ccagatatct tcagcgcggc ctccccgctc acggtctgct tattgagcta 300
gccccgctag ttctctgcac acgcttccac caataccagg cagacgactt ggtccgggac 360
tggcggggcca agctgcggga gttccagcag cagactcttc tgaatgctat gctgaaatcg 420
ctccaagagc ttgtggacag tcgggcgcgt tcgctgctg ctaggtcggc gggtcggcgt 480
ctcccagaaa gagtttcgag tccgacacgg ctggagaggt cggctgctat tgtaacagag 540
gaagaaccgg ctgctcctga aagagaggaa gaggaggaag aaagaggaga tagggaggac 600
gagcctgaac cagaacccga acctgaacct gaacttacct ccagccggtc atctacggag 660
acttctctgc cagccgttga ggctcatgtc gcggagccaa ccgttcctca gactgagtcc 720
agaagagtca ctgcgaaacc aatcgaagga gactgtacta tctgcctgtg tcctctacga 780
gaacaagaca gtgatgaaaa cggcgaggga tcagaagatc gcgatgatga gaatgaggat 840
gatgcggcgg gcacagggtc cggcacagcg tccgacgagc acgacgcccc cgaagaacat 900
gacgatgacg accttgtata ttgcaaaaac cagtgcggta cgaactatca caaagcctgt 960
attgacgtgt ggcattgctac tcagcgtaca tttgaaactc cacgtgggga tcctatcggc 1020
ctgtcctgcc cgtactgtcg agcagcatgg tcctcctga 1059

<210> 198
<211> 1059
<212> DNA
<213> *Aspergillus fumigatus*

<220>
<223> Homologue GmZnf1; Phylum CEA284.2;
contig 4899 region 477626-479684
Coding region without introns

<400> 198
atgtctgtgg ttgttcttgt ttccaagcca acagcacatt tctcagaatt ggcatctcat 60
cacagagtcc gtgtaattat cacattagca aaagccacaa tgtcccaccc cgatctatcg 120
accattctcg aggtctaccc cgaatgcgaa gtcacctgct acgggtacgc tcccagccaa 180
cggcgccgct gcagaatgcg aaccaggaaa gacaaccgag acagggcttc gtaccttctc 240
gaagagggca ccagatatct tcagcgcggc ctccccgctc acggtctgct tattgagcta 300
gccccgctag ttctctgcac acgcttccac caataccagg cagacgactt ggtccgggac 360
tggcggggcca agctgcggga gttccagcag cagactcttc tgaatgctat gctgaaatcg 420
ctccaagagc ttgtggacag tcgggcgcgt tcgctgctg ctaggtcggc gggtcggcgt 480
ctcccagaaa gagtttcgag tccgacacgg ctggagaggt cggctgctat tgtaacagag 540
gaagaaccgg ctgctcctga aagagaggaa gaggaggaag aaagaggaga tagggaggac 600
gagcctgaac cagaacccga acctgaacct gaacttacct ccagccggtc atctacggag 660
acttctctgc cagccgttga ggctcatgtc gcggagccaa ccgttcctca gactgagtcc 720
agaagagtca ctgcgaaacc aatcgaagga gactgtacta tctgcctgtg tcctctacga 780
gaacaagaca gtgatgaaaa cggcgaggga tcagaagatc gcgatgatga gaatgaggat 840
gatgcggcgg gcacagggtc cggcacagcg tccgacgagc acgacgcccc cgaagaacat 900

```

gacgatgacg accttggtata ttgcaaaaac cagtgcggtg cgaactatca caaagcctgt    960
attgacgtgt ggcattgtac tcagcgtaca tttgaaactc cacgtgggga tcctatcggc    1020
ctgtcctgcc cgtactgtcg agcagcatgg tcctcctga    1059

```

<210> 199

<211> 352

<212> PRT

<213> *Aspergillus fumigatus*

<220>

```

<223> Homologue GmZnf1; Phylum CEA284.2;
      contig 4899 region 477626-479684
      Protein sequence

```

<400> 199

```

Met Ser Val Val Val Leu Val Ser Lys Pro Thr Ala His Phe Ser Glu
1              5              10              15

Leu Ala Ser His His Arg Val Arg Val Ile Ile Thr Leu Ala Lys Ala
      20              25              30

Thr Met Ser His Pro Asp Leu Ser Thr Ile Leu Glu Val Tyr Pro Glu
      35              40              45

Cys Glu Val Thr Cys Tyr Gly Tyr Ala Pro Ser Gln Arg Arg Arg Cys
      50              55              60

Arg Met Arg Thr Arg Lys Asp Asn Arg Asp Arg Ala Ser Tyr Leu Leu
      65              70              75              80

Glu Glu Gly Thr Arg Tyr Leu Gln Arg Gly Leu Pro Val Asp Gly Leu
      85              90              95

Leu Ile Glu Leu Ala Pro Leu Val Leu Cys Thr Arg Phe His Gln Tyr
      100             105             110

Gln Ala Asp Asp Leu Val Arg Asp Trp Arg Ala Lys Leu Arg Glu Phe
      115             120             125

Gln Gln Gln Thr Leu Leu Asn Ala Met Leu Lys Ser Leu Gln Glu Leu
      130             135             140

Val Asp Ser Arg Ala Arg Ser Arg Ala Ala Arg Ser Ala Gly Arg Arg
      145             150             155             160

Leu Pro Glu Arg Val Ser Ser Pro Thr Arg Leu Glu Arg Ser Ala Ala
      165             170             175

Ile Val Thr Glu Glu Glu Pro Ala Ala Pro Glu Arg Glu Glu Glu Glu
      180             185             190

Glu Glu Arg Gly Asp Arg Glu Asp Glu Pro Glu Pro Glu Pro Glu Pro
      195             200             205

Glu Pro Glu Leu Thr Pro Ser Arg Ser Ser Thr Glu Thr Ser Ser Pro
      210             215             220

Ala Val Glu Ala His Val Ala Glu Pro Thr Val Pro Gln Thr Glu Ser
      225             230             235             240

```

Arg	Arg	Val	Thr	Arg	Lys	Pro	Ile	Glu	Gly	Asp	Cys	Thr	Ile	Cys	Leu	
				245					250					255		
Cys	Pro	Leu	Arg	Glu	Gln	Asp	Ser	Asp	Glu	Asn	Gly	Glu	Gly	Ser	Glu	
			260					265					270			
Asp	Arg	Asp	Asp	Glu	Asn	Glu	Asp	Asp	Ala	Ala	Gly	Thr	Gly	Ser	Gly	
		275					280					285				
Thr	Ala	Ser	Asp	Glu	His	Asp	Ala	Pro	Glu	Glu	His	Asp	Asp	Asp	Asp	
		290				295					300					
Leu	Val	Tyr	Cys	Lys	Asn	Gln	Cys	Gly	Thr	Asn	Tyr	His	Lys	Ala	Cys	
305					310					315					320	
Ile	Asp	Val	Trp	His	Ala	Thr	Gln	Arg	Thr	Phe	Glu	Thr	Pro	Arg	Gly	
				325					330					335		
Asp	Pro	Ile	Gly	Leu	Ser	Cys	Pro	Tyr	Cys	Arg	Ala	Ala	Trp	Ser	Ser	
			340					345					350			